

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 12, 2005, 06:38:28 ; Search time 184 Seconds
(without alignments)
1760.776 Million cell updates/sec

Title: US-09-508-832-10

Perfect score: 1065

Sequence: 1 MAKQPSDVSECDREGRLQ.....PRMVLRLRLRYIVRLWRMH 198

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USF0_spool_h/US09508832/runat_07112005_092436_425/app_query.fasta_1.391
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09508832 @CGN 1.1 69 @runat_07112005_092436_425 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFBLCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*

1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	713	66.9	44479	4	US-09-949-016-17176
2	695	65.4	417	4	Sequence 17176, A
3	332.5	31.2	477	4	Sequence 5434, Ap
4	323	30.3	398	4	Sequence 2099, Ap
5	192	18.0	601	4	Sequence 2153, Ap
6	125.5	11.8	1158	4	Sequence 189929, A
7	125.5	11.8	1455	4	Sequence 10541, A
8	125.5	11.8	2130	4	Sequence 10325, A
9	120.5	11.3	3433	4	Sequence 10734, A
10	120.5	11.3	3434	4	Sequence 6810, Ap
11	119.5	11.2	26314	4	Sequence 564, Ap
12	119.5	11.2	29927	4	Sequence 16389, A
					Sequence 11814, A

C 13	119.5	11.2	29927	4	US-09-949-016-17474	Sequence 17474, A
C 14	119.5	11.2	29927	4	US-09-949-016-17475	Sequence 17475, A
C 15	119.5	11.2	37802	4	US-09-949-016-12639	Sequence 12639, A
C 16	118.5	11.1	1167	4	US-09-902-540-3048	Sequence 3048, Ap
C 17	118.5	11.1	5895	4	US-09-902-540-792	Sequence 792, Ap
C 18	118.5	10.8	2553	4	US-09-902-540-2867	Sequence 2867, Ap
C 19	115.5	10.8	17592	4	US-09-902-540-1138	Sequence 1138, Ap
C 20	114	10.7	483	4	US-09-252-991A-10520	Sequence 10520, A
C 21	114	10.7	22123	4	US-09-949-016-12376	Sequence 12376, A
C 22	114	10.7	22124	4	US-09-949-016-14666	Sequence 14666, A
C 23	113	10.6	15789	4	US-09-902-540-1139	Sequence 1139, Ap
C 24	112	10.5	3492	4	US-09-902-540-3089	Sequence 3089, Ap
C 25	111.5	10.5	2258	4	US-09-016-434-1415	Sequence 1415, Ap
C 26	111.5	10.5	3705	2	US-08-474-379C-64	Sequence 64, Appl
C 27	111.5	10.5	3705	3	US-09-146-249A-64	Sequence 64, Appl
C 28	111.5	10.5	3705	3	US-08-206-188B-64	Sequence 64, Appl
C 29	111.5	10.5	3705	4	US-09-917-254-42	Sequence 42, Appl
C 30	111.5	10.5	6625	4	US-09-949-016-13334	Sequence 13334, A
C 31	111.5	10.5	17654	4	US-09-902-540-1161	Sequence 1161, Ap
C 32	111	10.4	601	4	US-09-949-016-38645	Sequence 38645, A
C 33	111	10.4	1981	4	US-09-949-016-1058	Sequence 1058, A
C 34	111	10.4	8521	4	US-09-949-016-12800	Sequence 12800, A
C 35	111	10.4	13117	4	US-09-949-016-15804	Sequence 15804, A
C 36	111	10.4	32010	4	US-09-949-016-13127	Sequence 13127, A
C 37	110.5	10.4	24459	4	US-09-902-540-5004	Sequence 5004, Ap
C 38	110.5	10.4	32241	4	US-09-902-540-1247	Sequence 1247, Ap
C 39	110	10.3	35784	4	US-09-949-016-16785	Sequence 16785, A
C 40	110	10.3	35784	4	US-09-949-016-16786	Sequence 16786, A
C 41	109.5	10.3	47476	4	US-09-949-016-12179	Sequence 12179, A
C 42	109.5	10.3	47476	4	US-09-949-016-14472	Sequence 14472, A
C 43	109	10.2	1419	4	US-09-902-540-5186	Sequence 5186, Ap
C 44	109	10.2	11854	4	US-09-902-540-1037	Sequence 1037, Ap
C 45	109	10.2	34094	4	US-09-292-034-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-949-016-17176
; Sequence 17176, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17176
; LENGTH: 44479
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(44479)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17176

Alignment Scores:
Pred. No.: 8,93e-53
Score: 713.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 66.95%
DB: 4
Length: 44479
Matches: 131
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-508-832-10 (1-198) x US-09-949-016-17176 (1-44479)

Qy 1 MetAlaIysGlnProSerAspValSerSerGluCysAspArgGluGlyArgGlnLeuGln 20
Db 2001 ATGGCAAAGCAACCTTCTGATGTAACTTCTGATGTGACCGAGAGGTAGACAATTGCAG 2060
Qy 21 ProAlaGluArgProGlnLeuArgProGlyAlaProThrSerLeuGlnThrGluPro 40
Db 2061 CCTCGGAGAGGCTCTCCACCTCAGACCTGGGGCCCTACTCTCCCTACACAGAGCCA 2120
Qy 41 GlnGlyAsnProGluGlyAsnHisGlyGlyGluGlyAspSerCysProHisGlySerPro 60
Db 2121 CAAGGTAATCTGAAGCAATCACGGAGGTGAAGGACAGCTGCCCCACGGCAGCCCT 2180
Qy 61 GlnGlyProLeuAlaProProAlaSerProGlyProPheAlaThrArgSerProLeuPhe 80
Db 2181 CAGGGCCGCTGGGCCACCTGCCAGCCCTGGCCCTTTTGTACAGATCCCGCTTTTC 2240
Qy 81 IlePheMetArgArgSerSerLeuLeuSerArgSerSerGlyTyrPheSerPheAsp 100
Db 2241 ATCTTTATGAGAAATCTCTCCCTGCTGCTCGATCTCCAGTGGGTATTTCTCTTTTGAC 2300
Qy 101 ThrAspArgSerProAlaProMetSerCysAspLysSerThrGlnThrProSerProPro 120
Db 2301 ACAGACAGAGCCCGACACCATCATGTTGTGACAAATCAACACAAACCCCAAGTCTCTCT 2360
Qy 121 CysGlnAlaPheAsnHisTyrLeuSerAlaMet 131
Db 2361 TGCCAGGCTTCAACCACTATCTCAGTGCATG 2393

RESULT 2

US-09-949-016-5434
; Sequence 5434, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5434
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5434

Alignment Scores:
Pred. No.: 5,01e-54 Length: 417
Score: 596.00 Matches: 138
Percent Similarity: 69.70% Conservative: 0
Best Local Similarity: 69.70% Mismatches: 0
Query Match: 65.35% Indels: 60
DB: 4 Gaps: 1

US-09-508-832-10 (1-198) x US-09-949-016-5434 (1-417)

Qy 1 MetAlaIysGlnProSerAspValSerSerGluCysAspArgGluGlyArgGlnLeuGln 20
Db 1 ATGGCAAAGCAACCTTCTGATGTAACTTCTGATGTGACCGAGAGGTAGACAATTGCAG 60
Qy 21 ProAlaGluArgProGlnLeuArgProGlyAlaProThrSerLeuGlnThrGluPro 40
Db 61 CCTCGGAGAGGCTCTCCACCTCAGACCTGGGGCCCTACTCTCCCTACACAGAGCCA 120

Qy 41 GlnGlyAsnProGluGlyAsnHisGlyGlyGluGlyAspSerCysProHisGlySerPro 60
Db 121 CAA----- 123
Qy 61 GlnGlyProLeuAlaProProAlaSerProGlyProPheAlaThrArgSerProLeuPhe 80
Db 123 ----- 123
Qy 81 IlePheMetArgArgSerSerLeuLeuSerArgSerSerGlyTyrPheSerPheAsp 100
Db 123 ----- 123
Qy 101 ThrAspArgSerProAlaProMetSerCysAspLysSerThrGlnThrProSerProPro 120
Db 124 ---GACAGGAGCCAGCACCATGAGTTGTGACAAATCAACACAAACCCCAAGTCTCTCT 180
Qy 121 CysGlnAlaPheAsnHisTyrLeuSerAlaMetAlaSerMetArgGlnAlaGluProAla 140
Db 181 TGCCAGGCTTCAACCACTATCTCAGTGCATGCGTTCATGAGGACGGCTGAACCTGCA 240
Qy 141 AspMetArgProGluLleThrPheAlaGlnGluLeuArgArgIleGlyAspGluPheAsn 160
Db 241 GATATGCGCCAGAGATATGATCGCCCAAGAGTTGCGGCGTATCGGAGACGAGTTTAAAC 300
Qy 161 AlaTyrTyrAlaArgArgValPheLeuAsnAsnTyrGlnAlaAlaGluAspHisProArg 180
Db 301 GCTTACTATGCAAGGAGGGTATTTTGAATAATATACCAAGCAGCCGAAGACCCACGCA 360
Qy 181 MetValIleLeuArgLeuLeuArgTyrIleValArgLeuValTyrArgMetHis 198
Db 361 ATGGTTATCTTACGACTGTTCAGTTACGTTGCGCTCGTGTGGAGAATGCAT 414

RESULT 3

US-09-621-976-2099
; Sequence 2099, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2099
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 223..372
US-09-621-976-2099

Alignment Scores:
Pred. No.: 2,87e-21 Length: 477
Score: 332.50 Matches: 76
Percent Similarity: 48.12% Conservative: 1
Best Local Similarity: 47.50% Mismatches: 5
Query Match: 31.22% Indels: 78
DB: 4 Gaps: 2

US-09-508-832-10 (1-198) x US-09-621-976-2099 (1-477)

Qy 1 MetAlaIysGlnProSerAspValSerSerGluCysAspArgGluGlyArgGlnLeuGln 20
Db 223 ATGGCAAAGCAACCTTCTGATGTAACTTCTGATGTGACCGAGAGGTAGACAATTGCA 282
Qy 20 nProAlaGluArgProGlnLeuArgProGlyAlaProThrSerLeuGlnThrGluPr 40
Db 283 GCCTGCGAGAGGCTCTCCACCTCAGACCTGGGGCCCTACTCTCCCTACACAGAGGCC 342

QY 40 oGlnGlyAsnProGluGlyAsnHisGlyGlyGluGlyAspSerCysProHisGlySerPr 60
Db 343 ACNA----- 346
QY 60 oGlnGlyProLeuAlaProProAlaSerProGlyProPheAlaThrArgSerProLeuPh 80
Db 346----- 346
QY 80 ellePheMetArgArgSerSerLeuLeuSerArgSerSerGlyTyrrPheSerPheAs 100
Db 346----- 346
QY 100 pThrAspArgSerProAlaProMetSerCysAspLysSerThrGlnThrProSerProPr 120
Db 347 ----GACAGAGGCCAGCACCAGTGGTGTGACAAATCAACACAAACCCAGTCTCTC 402
QY 120 oCysGlnAlaPheAsnHisTyrrLeuSerAlaMetAlaSerMetArgGlnAlaGluProAl 140
Db 403 TTGCCAGGCCCTTCAACCACTATCTCAGTGCATGTAGTATC----- 445
QY 140 aAspMetArgProGluLeuTrpIleAlaGlnGluLeuArgArgIleGlyAspGluPhe 159
Db 446 -----CTAGAGGATATAGGTGATCTTTTC 469

RESULT 4
US-09-621-976-2153
; Sequence 2153, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2153
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 18..239
; NAME/KEY: misc_feature
; LOCATION: 14
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-2153

Alignment Scores:
Pred. No.: 1.6e-20 Length: 398
Score: 323.00 Matches: 58
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 30.33% Indels: 0
DB: 4 Gaps: 0
US-09-508-832-10 (1-198) x US-09-621-976-2153 (1-398)
QY 1 MetalAlaGlnProSerAspValSerSerGluCysAspArgGluGlyArgGlnLeuGln 20
Db 223 ATGCAAGCAACCTTCTGATGTAAAGTTCTGAGTGTGACCGAGAGAGGTAGACAATTGCAG 282
QY 21 ProAlaGluArgProProGlnLeuArgProGlyAlaProThrSerLeuGlnThrGluPro 40
Db 283 CTTGCGAGAGGGCTCCCGAGCTCAGACCTGGGGCCCTACCTCCCTACACAGAGAGCCA 342
QY 41 GlnGlyAsnProGluGlyAsnHisGlyGlyGluGlyAspSerCysProHisGly 58
Db 343 CAAGGTAACTCTGAAGCAATACCGGAGGTGAAGGGGACAGCTGCCCCCAGCGC 396

RESULT 5
US-09-949-016-189929
; Sequence 189929, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 189929
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-189929

Alignment Scores:
Pred. No.: 1.68e-08 Length: 601
Score: 192.00 Matches: 37
Percent Similarity: 90.70% Conservative: 2
Best Local Similarity: 86.05% Mismatches: 4
Query Match: 18.03% Indels: 0
DB: 4 Gaps: 0
US-09-508-832-10 (1-198) x US-09-949-016-189929 (1-601)

QY 127 TyrLeuSerAlaMetAlaSerMetArgGlnAlaGluProAlaAspMetArgProGluIle 146
Db 215 TTTTGTCTGATGCAGCTTCCATGAGCGCAGGCTGACCTGCAGATATGCCCGCAGATA 274
QY 147 TrpIleAlaGlnGluLeuArgArgIleGlyAspGluPheAsnAlaTyrrAlaAspArg 166
Db 275 TGGATCGCCCAAGATTGCGCGTATYGAGACAGAGTTTAACTTACTACTGCAAGGAGG 334
QY 167 ValPheLeu 169
Db 335 GTAATGATG 343

RESULT 6
US-09-252-991A-10541/c
; Sequence 10541, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 10541
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10541
Alignment Scores:
Pred. No.: 0.0393 Length: 1158
Score: 125.50 Matches: 55
Percent Similarity: 37.10% Conservative: 14

Best Local Similarity: 29.57% Mismatches: 67
 Query Match: 11.78% Indels: 50
 DB: 4 Gaps: 9

US-09-508-832-10 (1-198) x US-09-252-991A-10541 (1-1158)

QY 21 ProAlaGluArgProGlnLeuArgProGly-----AlaProThrSerLeuGln 37
 DB 814 CCTCGACGAAAGCGCGCGCCGAGCCAGGCGCTGCGTCCGCGCAGGTGCGCTGCC 755
 QY 38 ThrGluProGlnGly-----AsnProGluGlyAsnHis-----Gly 49
 DB 754 AGCGTCCAGTGGCGCGCTGGAATGCCCTCCAGGAGCCATCGGCCGCGCGCCGC 695
 QY 50 GlyGluGlyAspSerCysProHisGlySerProGlnGlyProLeuAlaProAlaSer 69
 DB 694 GGTTCAGGCTCCAGCGCAACTCCAGGTTTCGGTGGCGCGCCAGCGCTCCAGTCCG 635
 QY 70 ProGlyProPheAlaThrArgSerProLeuPheIlePheMetArgSerSerLeu 89
 DB 634 CGAGCCAGGCGCGCTGCGCGGATGAC-----GGACGTAGTCAGCCACA 590
 QY 90 SerArgSerSerGlyTyrPheSerPheAspThrAsp---ArgSerProAlaProMet 108
 DB 589 GCACGG-----GACCGCATAGCGTTCTCCAGCGCTCCG 554
 QY 109 Ser-----CysAspLysSerThrGlnThrProSerPro 119
 DB 553 GGAGCAGCGCGAGCAAGCGCTCAGCGCGTTCGCGGCGCCAGCAGCGCCCTCGG 494
 QY 120 ProCysGlnAlaPheAsnHisTyrLeuSerAlaMetAlaSerMetArgGlnAlaGluPro 139
 DB 493 CCTGCATCGCGCAGCGCAGATCGCTTCGCGGGTTCGCAACTCGACACGCTGCGCGCCG 434
 QY 140 AlaAspMetArgProGluIleTyrPheIleAlaGlnLeuArgGlyAspGluPhe 159
 DB 433 CCAGGTGTCGCACAACC----- 416
 QY 160 AsnAlaTyrTyrAlaArg-ArgValPheLeuAsn---AsnTyrGlnAlaAlaGluAspHi 178
 DB 415 AGGCGAGAGCAGCGCGCTCGCGGTGAGCTTGACGGCGATTTCCAGCGCGCTCGCGCACCA 356
 QY 178 sProArgMetValile 183
 DB 355 CCGGGTCAGGCTGTA 340

RESULT 7

US-09-252-991A-10325
 ; Sequence 10325, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 10325
 ; LENGTH: 1455
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-10325

Alignment Scores:
 Pred. No.: 0.0538 Length: 1455
 Score: 125.50 Matches: 55
 Percent Similarity: 37.10% Conservative: 14
 Best Local Similarity: 29.57% Mismatches: 67

Query Match: 11.78% Indels: 50
 DB: 4 Gaps: 9

US-09-508-832-10 (1-198) x US-09-252-991A-10325 (1-1455)

QY 21 ProAlaGluArgProGlnLeuArgProGly-----AlaProThrSerLeuGln 37
 DB 624 CCTCGACGAAAGCGCGCGCCGAGCCAGGCGCTGCGTCCGCGCAGGTGCGCTGCC 683
 QY 38 ThrGluProGlnGly-----AsnProGluGlyAsnHis-----Gly 49
 DB 684 AGCGTCCAGTGGCGCGCTGGAATGCCCTCCAGGAGCCATCGGCCGCGCGCCGC 743
 QY 50 GlyGluGlyAspSerCysProHisGlySerProGlnGlyProLeuAlaProAlaSer 69
 DB 744 GGTTCAGGCTCCAGCGCAACTCCAGGTTTCGGTGGCGCGCCAGCGCTCCAGTCCG 803
 QY 70 ProGlyProPheAlaThrArgSerProLeuPheIlePheMetArgSerSerLeu 89
 DB 804 CGAGCCAGGCGCGCTGCGCGGATGAC-----GGACGTAGTCAGCCACA 848
 QY 90 SerArgSerSerGlyTyrPheSerPheAspThrAsp---ArgSerProAlaProMet 108
 DB 849 GCACGG-----GACCGCATAGCGTTCTCCAGCGCTCCG 884
 QY 109 Ser-----CysAspLysSerThrGlnThrProSerPro 119
 DB 885 GGAGCAGCGCGAGCAAGCGCTCAGCGCGTTCGCGGCGCCAGCAGCGCCCTCGG 944
 QY 120 ProCysGlnAlaPheAsnHisTyrLeuSerAlaMetAlaSerMetArgGlnAlaGluPro 139
 DB 945 CCTGCATCGCGCAGCGCAGATCGCTTCGCGGGTTCGCAACTCGACACGCTGCGCGCCG 1004
 QY 140 AlaAspMetArgProGluIleTyrPheIleAlaGlnLeuArgGlyAspGluPhe 159
 DB 1005 CCAGGTGTCGCACAACC----- 1022
 QY 160 AsnAlaTyrTyrAlaArg-ArgValPheLeuAsn---AsnTyrGlnAlaAlaGluAspHi 178
 DB 1023 AGGCGAGAGCAGCGCGCTCGCGGTGAGCTTGACGGCGATTTCCAGCGCGCTCGCGCACCA 1082
 QY 178 sProArgMetValile 183
 DB 1083 CCGGGTCAGGCTGTA 1098

RESULT 8
 US-09-252-991A-10734/c
 ; Sequence 10734, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 10734
 ; LENGTH: 2130
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-10734

Alignment Scores:
 Pred. No.: 0.0906 Length: 2130
 Score: 125.50 Matches: 55
 Percent Similarity: 37.10% Conservative: 14
 Best Local Similarity: 29.57% Mismatches: 67
 Query Match: 11.78% Indels: 50

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DB: 4 Gaps: 9
US-09-508-832-10 (1-198) x US-09-252-991A-10734 (1-2130)
QY 21 ProAlaGluArgProGlnLeuArgProGly-----AlaProThrSerLeuGln 37
DB 677 CCTCGACGAAGCGCGCGCCGCGCAGCGCCGCGCTGGCTGCGCGCCGCTGCGCC 618
QY 38 ThrGluProGlnGly-----AsnProGluGlyAsnHis-----Gly 49
DB 617 AGCCGTCACGAGTGGCGCGCTGGAAATGCCCTCCAGGAGCATCGGCCCGCGCCCGC 558
QY 50 GlyGluGlyAspSerCysProHisGlySerProGlnGlyProLeuAlaProProAlaSer 69
DB 557 GGTCTCAGGCTCCAGCGCAATCTCAGGTTGCGGTGGCGCGCGCCAGCGCTCCAGCTCGC 498
QY 70 ProGlyProPheAlaThrArgSerProLeuPheIlePheMetArgArgSerSerLeuLeu 89
DB 497 CGAGCCAGGCGCGCTGGCCGGGATGAC-----GGAGCTAGTGCGAGCCACA 453
QY 90 SerArgSerSerSerGlyTyrPheSerPheAspThrAsp---ArgSerProAlaProMet 108
DB 452 GCACGG-----GACCGGATAGCGTCTCCAGCGCTCGC 417
QY 109 Ser-----CysAspLysSerThrGlnThrProSerPro 119
DB 416 GGAGCAGGCGCGCAGCAAGGCGCTCAGCGCGTGGCGCGCAGCAGCGCGCTCGG 357
QY 120 ProCysGlnAlaPheAsnHisTyrLeuSerAlaMetAlaSerMetArgGlnAlaGluPro 139
DB 356 CTGTCATCGCGCCAGCGAGTCGCCCTTGGCGGGTTGCACTCGACACGCTGGCCGACCG 297
QY 140 AlaAspMetArgProGluIleTyrPheAlaGlnGluLeuArgArgIleGlyAspGluPhe 159
DB 296 CCAGGTGTTCGCACACC-----279
QY 160 AsnAlaTyrTyrAlaArg-ArgValPheLeuAen---AsnTyrGlnAlaAlaGluAspHi 178
DB 278 AGGCGCAGAGCAGCGCGCTCGCGGTGACGCTTGACGGCGATTTCCAGCGCGTCCGCCGACCA 219
QY 178 sProArgMetValle 183
DB 218 CCCGGGTACGGCTGTA 203

RESULT 9
US-09-508-832-10 (1-198) x US-09-252-991A-10734 (1-2130)
; Sequence 6810, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 6810
; LENGTH: 3433
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-508-832-10 (1-198) x US-09-902-540-6810 (1-3433)
QY 21 ProAlaGluArgProPro-----GlnLeuArgProGlyAlaPro 33
DB 2203 CCAGCAACTCGGCACACCATGCGAGCCATGCGAGCTCGGAGCGTAGGCGAGCTCAAGC 2144
QY 34 ThrSerLeuGlnThrGluProGlnGlyAsnProGluGlyAsnHisGlyGlyGluGlyAsp 53
DB 2143 GCAGCGTGTCCCGGGAACCA-----CATAGGCAATGAGCGGT 2105
QY 54 SerCysPro---HisGlySerProGlnGlyProLeuAlaProProAlaSerProGlyPro 72
DB 2104 GGTTCGCTGTCTCAGCGCTCTCAGCTCCACCATCTCCAGCCCGGCGACCGCTGTCCCA 2045
QY 73 PheAlaThrArgSerProLeuPheIlePheMetArgArgSerSerLeuLeuSerArgSer 92
DB 2044 GCAGGTGTCCGAGCGAT-----AGTCTCGAAGATGAGCAGGCTCTCGAAA 1997
QY 93 SerSerGlyTyrPheSerPheAspThrAspArgSerProAlaProMetSerCysAspLys 112
DB 1996 GCGGAGCGCGCGAGCATGCTCCAGCCCTTCACTGGACCGCGGAGTGTGCTCGT 1937
QY 113 SerThrGlnThrProSerProCysGlnAlaPheAsnHisTyrLeuSerAlaMetAla 132
DB 1936 ACTTCGCGATCTCCAGCT-----GCCGTGCTGGAGCT 1904
QY 133 SerMetArgGlnAlaGluProAlaAspMetArg-----ProGluIleTyrPheAlaGln 150
DB 1903 TCTGAGCAGCGCGCAGCAGCGGCTTGGAGGAGCAGCCCGCGGATGGCGAGCGAGT 1844
QY 151 -----GluLeuArgArgIleGly-----AspGluPheAsnAla 161
DB 1843 TGATGAACAGGCGCCACCATGAGCTCGCGCTCTGGCAGGTCCACGGGAGCGCGAGACTG 1784
QY 162 TyrTyrAlaArg-ValPheLeuAsnAsnTyrGlnAlaAlaGluAspHiProArgMe 181
DB 1783 TGGCGCGGAGAGCAGCGCTCTCTGCGCGCATGCGCGCGCGAGGAGCAGCGCCACCGCG 1724
QY 181 tValleLeuArgLeuLeuArgTyrIleVal 191
DB 1723 CCTGCGTACGCGTGTGAGCGTTCACCGCGTT 1693

RESULT 10
US-09-902-540-6810/c
; Sequence 564, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 564
; LENGTH: 3434
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-6810

Alignment Scores:
Pred. No.: 0.491 Length: 3434
Score: 120.50 Matches: 54
Percent Similarity: 38.74% Conservative: 20
Best Local Similarity: 28.27% Mismatches: 77
Query Match: 11.31% Indels: 40
DB: 4 Gaps: 8
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US-09-508-832-10 (1-198) x US-09-949-016-11814 (1-29927)

Qy	9	SerSerGluCysAspArgGluGlyArg-----GlnLeuGlnProAlaGluArgPro	26
Db	20801	TCCCCAAGCCTCTCCCGGAGACACCAAGGTGTCCAAGCCTCTCCGGGTCA	20742
Qy	27	GlnLeu-----ArgProGlyAlaProThrSerLeuGln---Thr-GluProGlnG	42
Db	20741	AGGCTCTCTCCCGAGACACCAAGGTCCCCCAGCCTCTCCCCAGGACACCA	20682
Qy	42	AsnProGlu-----GlyAsnHisGlyGlyG	51
Db	20681	CTCTCCCGAGACACCAAGGTCCCCAAGCCTCTCCCGGAGACACCAAGGT	20622
Qy	51	uGlyAspSerCysProHisGlySerProGln-----GlyProLeuAlaPro	69
Db	20621	CGGTCACCTAGGTCCCCCAAGGCACCTCCGAGACACCAAGTCTCCCAAG	20562
Qy	69	rProGlyProPheAla-----ThrArgSerProLeuPheIlePheMetArg	85
Db	20561	ACCAGGTCCCGCAAGGTCTCTCCCGAGACACCAAGTCTCCCAAGGTCT	20502
Qy	85	gSerSerLeuLeuSerArg-----SerSerSerGlyTyrPheSerPheAsp	101
Db	20501	GTCCCCAGGCCTCTCCAGGTACACAGGTCCCCAAGCCTCTCTCGGACAC	20442
Qy	102	-----AspArg-SerProAlaProMetSerCysAspLysSerThrGlnThr	117
Db	20441	AAGCCTCTCCCGGACACCAAGTCCCAAGCC-----TCTCCGGGACACCA	20391
Qy	118	-----SerProProCysGlnAlaPheAsnHisTyrLeuSerAlaMet	132
Db	20390	CCCAAGCCTCTCCCGCTCACCAGATCTCCAAGCCTCTCCAGGACACCAAG	20331
Qy	132	laSerMetArg-----GlnAlaGluProAlaAspMetArg	143
Db	20330	CTCTCCCCAGGACACCAAGTCCCCAAGCCTCTCTCCCGAGACACCAAG	20284

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RESULT 13
US-09-949-016-17474/c
; Sequence 17474, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17474
; LENGTH: 29927
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(29927)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17474

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Alignment Scores:		
Pred. No.:	11.7	Length: 29927
Score:	119.50	Matches: 60
Percent Similarity:	41.24%	Conservative: 13
Best Local Similarity:	33.90%	Mismatches: 59
Query Match:	11.22%	Indels: 45

DB:	4	Gaps:	11
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US-09-508-832-10 (1-198) x US-09-949-016-17474 (1-29927)

QY   9 SerSerGluCysAspArgGluGlyArg-----GlnLeuGlnProAlaGluArgProPro 26
Db   20801 TCCCAAGCCTCTCCCGGGACACCAGGTGTCCAAGCTTCTCCGGGTCAACAGGTCCCCA 20742

QY   27 GlnLeu-----ArgProGlyAlaProThrSerLeuGln---Thr-GluProGlnGl 42
Db   20741 AGGCTCTCTCCGAGACACCAGGTCCCAGCCTCTCCCCAGGACACCAGATCCCCAAG 20682

QY   42 yAasnProGlu-----GlyAasnHisGlyGlyGl 51
Db   20681 CTCTCCCAAGGACACCAGGTCCCCAAGCCTCTCCCGGGACACCAGGTCCCCAAGCCTCTCC 20622

QY   51 uGlyAspSerCysProHisGlySerProGln-----GlyProLeuAlaProProAlase 69
Db   20621 CGGGTCAC TAGGTCCCCAAGGCATCTCCGAGACACCAGGTCTCCCAAGCCTCTCCAAGGTC 20562

QY   69 rProGlyPropheAla-----ThrArgSerProLeuPheIlePheMetArgAr 85
Db   20561 ACCAGTCCCCAAGGCTCTCCCAAGGACACCAGGTCCCCAAGGTCTCTCCGGGTCAACCAG 20502

QY   85 gSerSerLeuLeuSerArg--SerSerSerGlyTyzrPheSerPheaspThr----- 101
Db   20501 GTCCCAAGCCTCTCCAAGGTCAACAGGTCCCAAGTCCCAAGCCTCTCTGGGACACCAGGTGTCC 20442

QY   102 -----AspArg-SerProAlaProMetSerCysAspLysSerThrGlnThrPro--- 117
Db   20441 AAGCCTCTCCCGGGACACCAAGTCCCCAAGCC-----TCTCCGGGACACCAGGTCTCC 20391

QY   118 -----SerProProCysGlnAlaPheAsnHisTyrLeuSerAlaMeta 132
Db   20390 CCCAAGCCTCTCCGGCTCACCATGATCTCAAGCCTCTCCCAAGGACACCAGGTCCCCAAG 20331

QY   132 laSerMetArg-----GlnAlaGluProAlaAspMetArg 143
Db   20330 CTTCTCCCAAGACACCAGGTCCCCAAGCCTCTCTCCCAAGGACACCAGGTCCCCAAG 20284

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RESULT 14

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US-09-949-016-17475/c
; Sequence 17475, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17475
; LENGTH: 29927
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(29927)
; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-17475

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Alignment Scores:		
Pred. No.:	11.7	29927
Score:	119.50	60
Percent Similarity:	41.24%	Conservative: 13

Best Local Similarity: 33.90% Mismatches: 59
Query Match: 11.22% Indels: 45
DB: 4 Gaps: 11
US-09-508-832-10 (1-198) x US-09-949-016-17475 (1-29927)

QY 9 SerSerGluCysAspArgGluGlyArg-----GlnLeuGlnProAlaGluArgProPro 26
Db 20801 TCCCAAGCCTCTCCCGGACACCAAGGTGTCCAAGCCTCTCCCGGGTCCACAGGTCCCCA 20742
QY 27 GlnLeu-----ArgProGlyAlaProThrSerLeuGln---Thr-GluProGlnG1 42
Db 20741 AGGCTCTCTCCGAGACACCAAGGTCCCCAGCCTCTCTCCGAGACACCAAGTCCCCAAGG 20682
QY 42 YAsnProGlu-----GlyAsnHisGlyGlyG1 51
Db 20681 CTCTCCGAGACACCAAGGTCCCCAAGCCTCTCCCGGACACCAAGGTCCCCAAGCCTCTCC 20622
QY 51 uGlyAspSerCysProHisGlySerProGln-----GlyProLeuAlaProProAlaSe 69
Db 20621 CGGGTCACTAGGTCCCCAAGGCACCTCCCGAGACACCAAGGTCCCCAAGCCTCTCCAAGGTC 20562
QY 69 rProGlyProPheAla-----ThrArgSerProLeuPheIlePheMetArgAr 85
Db 20561 ACCAGGTCCCCAAGGTCTCCCGAGACACCAAGGTCCCCAAGGTCTCCCGGGTCCACCAG 20502
QY 85 gSerSerLeuLeuSerArg---SerSerSerGlyTyrrPheSerPheAspThr----- 101
Db 20501 GTCCCCAGGCTCTCCAAGGTCCACAGGTCCCCAAGCCTCTCTGGGACACCAAGGTGTCC 20442
QY 102 -----AspArg-SerProAlaProMetSerCysAspLysSerThrGlnThrPro----- 117
Db 20441 AAGCCTCTCCCGGACACCAAGTCCCCAAGC-----TCTCCCGGACACCAAGGTC 20391
QY 118 -----SerProCysGlnAlaPheAsnHisTyrrLeuSerAlaMeta 132
Db 20390 CCCAAGCCTCTCCCGGTCCACAGATCTCCAAGCCTCTCCGAGACACCAAGGTCCCCAAG 20331
QY 132 laSerMetArg-----GlnAlaGluProAlaAspMetArg 143
Db 20330 CCTCTCCGAGACACCAAGGTCCCCAAGCCTCTCCCGAGACACCAAGG 20284

RESULT 15

US-09-949-016-12639/c
; Sequence 12639, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12639
; LENGTH: 37802
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(37802)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12639

Alignment Scores:

Pred. No.: 16.2 Length: 37802

Score: 119.50 Matches: 60
Percent Similarity: 41.24% Conservative: 13
Best Local Similarity: 33.90% Mismatches: 59
Query Match: 11.22% Indels: 45
DB: 4 Gaps: 11
US-09-508-832-10 (1-198) x US-09-949-016-12639 (1-37802)

QY 9 SerSerGluCysAspArgGluGlyArg-----GlnLeuGlnProAlaGluArgProPro 26
Db 20801 TCCCAAGCCTCTCCCGGACACCAAGGTGTCCAAGCCTCTCCCGGGTCCACAGGTCCCCA 20742
QY 27 GlnLeu-----ArgProGlyAlaProThrSerLeuGln---Thr-GluProGlnG1 42
Db 20741 AGGCTCTCTCCGAGACACCAAGGTCCCCAGCCTCTCTCCGAGACACCAAGTCCCCAAGG 20682
QY 42 YAsnProGlu-----GlyAsnHisGlyGlyG1 51
Db 20681 CTCTCCGAGACACCAAGGTCCCCAAGCCTCTCCCGGACACCAAGGTCCCCAAGCCTCTCC 20622
QY 51 uGlyAspSerCysProHisGlySerProGln-----GlyProLeuAlaProProAlaSe 69
Db 20621 CGGGTCACTAGGTCCCCAAGGCACCTCCCGAGACACCAAGGTCCCCAAGCCTCTCCAAGGTC 20562
QY 69 rProGlyProPheAla-----ThrArgSerProLeuPheIlePheMetArgAr 85
Db 20561 ACCAGGTCCCCAAGGTCTCCCGAGACACCAAGGTCCCCAAGGTCTCCCGGGTCCACCAG 20502
QY 85 gSerSerLeuLeuSerArg---SerSerSerGlyTyrrPheSerPheAspThr----- 101
Db 20501 GTCCCCAGGCTCTCCAAGGTCCACAGGTCCCCAAGCCTCTCTGGGACACCAAGGTGTCC 20442
QY 102 -----AspArg-SerProAlaProMetSerCysAspLysSerThrGlnThrPro----- 117
Db 20441 AAGCCTCTCCCGGACACCAAGTCCCCAAGC-----TCTCCCGGACACCAAGGTC 20391
QY 118 -----SerProCysGlnAlaPheAsnHisTyrrLeuSerAlaMeta 132
Db 20390 CCCAAGCCTCTCCCGGTCCACAGATCTCCAAGCCTCTCCGAGACACCAAGGTCCCCAAG 20331
QY 132 laSerMetArg-----GlnAlaGluProAlaAspMetArg 143
Db 20330 CCTCTCCGAGACACCAAGGTCCCCAAGCCTCTCCCGAGACACCAAGG 20284

Search completed: November 12, 2005, 06:48:29
Job time : 223 secs

GenCore version 5.1.6
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(without alignments)
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Searched: 9794790 seqs, 413490567 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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SUMMARIES

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3	497	46.7	442	24	US-10-450-763-1154
4	437	41.0	403	10	US-09-918-995-36495
5	192	18.0	455	14	US-10-027-632-75254
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7	192	18.0	455	18	US-10-027-632-75254
8	192	18.0	455	18	US-10-027-632-313542
9	189.5	17.8	199	15	US-10-092-750-72
10	178	16.7	105	15	US-10-092-750-153
11	125.5	11.8	1101	18	US-10-282-122A-7256
12	121.5	11.4	1933	20	US-10-437-963-96145
13	120.5	11.3	147223	24	US-10-981-277-21
14	120.5	11.3	151882	24	US-10-981-277-22
15	119.5	11.2	32367	15	US-10-158-160A-14
16	118.5	11.1	836	21	US-10-425-115-11764
17	117.5	11.0	2166	20	US-10-437-963-35782
18	116.5	10.9	9025608	16	US-10-156-761-1
19	116	10.9	557	21	US-10-425-115-148175
20	116	10.9	672	20	US-10-767-701-13103
21	116	10.9	759	19	US-10-240-425-590
22	115.5	10.8	862	20	US-10-767-701-3261
23	115.5	10.8	2544	18	US-10-369-493-43062
24	115	10.8	780	16	US-10-156-761-2892
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27	114.5	10.8	1305	16	US-10-156-761-3516
28	114	10.7	1785	20	US-10-437-963-92703
29	114	10.7	2317	11	US-09-764-875-294
30	114	10.7	2847	20	US-10-437-963-89518
31	113.5	10.7	893	21	US-10-425-115-71067
32	113	10.6	2345	18	US-10-310-154-287
33	113	10.6	2345	22	US-10-732-923-179
34	112.5	10.6	1123	21	US-10-425-115-701
35	112.5	10.6	2862	20	US-10-437-963-6992
36	112.5	10.6	3608	22	US-10-887-553A-633
37	112	10.5	1191	20	US-10-437-963-58554
38	112	10.5	1958	22	US-10-488-056-17
39	112	10.5	2370	24	US-10-450-763-20228
40	112	10.5	15738	17	US-10-329-079-12
41	112	10.5	37360	17	US-10-329-079-6
42	111.5	10.5	1116	17	US-10-214-446-5
43	111.5	10.5	1726	20	US-10-645-190-3
44	111.5	10.5	2258	9	US-09-964-824A-261
45	111.5	10.5	2258	18	US-10-305-720-1415

ALIGNMENTS

RESULT 1

US-10-755-889-15
; Sequence 15, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755.889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757

```
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: Patent version 3.2
; SEQ ID NO 15
; LENGTH: 826
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-755-889-15

Alignment Scores:
Pred. No.: 4,996-65 Length: 826
Score: 696.00 Matches: 138
Percent Similarity: 69.70% Conservative: 0
Best Local Similarity: 69.70% Mismatches: 0
Query Match: 65.35% Indels: 60
DB: 20 Gaps: 1

US-09-508-832-10 (1-198) x US-10-755-889-15 (1-826)

QY 1 MetAlaLysGlnProSerAspValSerSerGluCysAspArgGluGlyArgGlnLeuGln 20
Db 1 ATGGCAAGCAACCTTCTGATTAAGTCTGAGTGTGACCGAGAAGGTAGACAATTGCAG 60
QY 21 ProAlaGluArgProGlnLeuArgProGlyAlaProThrSerLeuGlnThrGluPro 40
Db 61 CTGCGGAGAGCCCTCCAGCTCAGACTGGGGCCCTACTCTCCCTACAGACAGGCCA 120
QY 41 GlnGlyAenProGluGlyAenHisGlyGlyGluGlyAenSerCysProHisGlySerPro 60
Db 121 CAA----- 123
QY 61 GlnGlyProLeuAlaProAlaSerProGlyProPheAlaThrArgSerProLeuPhe 80
Db 123 ----- 123
QY 81 IlePheMetArgSerSerLeuLeuSerArgSerSerSerGlyTyrPheSerPheAsp 100
Db 123 ----- 123
QY 101 ThrAspArgSerProAlaProMetSerCysAspLysSerThrGlnThrProSerProPro 120
Db 124 ---GACAGAGGCCAGCACCATGATGTTGTGACAAATCAACAAACCCCAAGTCTCTCT 180
QY 121 CysGlnAlaPheAenHisTyrLeuSerAlaMetAlaSerMetArgGlnAlaGluProAla 140
Db 181 TGCCAGGCCCTCAACCACTATCTCAGTGCATGCAATGGCTTCCATGAGGAGGCTGAACCTGCA 240
QY 141 AspMetArgProGluIleTyrIleAlaGlnGluLeuArgArgIleGlyAspGluPheAen 160
Db 241 GATATGGCCAGAGATATGGATCGCCCAAGAGTTGGCGGTATTGGAGACCGAGTTTAAAC 300
QY 161 AlaTyrTyrAlaArgArgValPheLeuAenAenTyrGlnAlaGluAenHisProArg 180
Db 301 GCTTACTATGCAAGGAGGTATTTTGAATAATTACCAAGCAGCCGAGACCAACCCACCA 360
QY 181 MetValIleLeuArgLeuLeuArgTyrIleValArgLeuValTyrArgMethHis 198
Db 361 ATGGTTATCTTACGACTGTACGTATCATTTGCCGCTCGTGTGGAGAATGCAT 414

RESULT 2
US-09-918-995-31159
; Sequence 31159, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054

US-10-450-763-1154
; Sequence 1154, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 1154
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (167)-(442)
; OTHER INFORMATION: 100% homologous to Homo sapiens BimEL, accession number
; OTHER INFORMATION: AF032457, Smith-Waterman Score=497.

US-10-450-763-1154
```

```
Alignment Scores:
Pred. No.: 6 21e-44 Length: 442
Score: 497.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 46.67% Indels: 0
DB: 24 Gaps: 0

US-09-508-832-10 (1-198) x US-10-450-763-1154 (1-442)

Qy 1 MetAlaYsGlnProSerAspValSerSerGluCyAspArgGluGlyArgGlnLeuGln 20
Db 167 ATGCCAAAGCAACCTTCTGATGAAGTCTCAGTGTGACCGAGAGGAGGTAGACAATTGCAG 226
Qy 21 ProAlaGluArgProProGlnLeuArgProGlyAlaProThrSerLeuGlnThrGluPro 40
Db 227 CCTCGGAGAGGCGCTCCACAGCTCAGACCTGGGGCCCTTACTCTCCCTACACAGAGCCA 286
Qy 41 GlnGlyAenProGluGlyAsnHisGlyGlyGluGlyAspSerCysProHisGlySerPro 60
Db 287 CAAGGTAACTCTGAAGCAATACGGAGGTGAGGGGACAGCTGCCCGCCAGCGCCTT 346
Qy 61 GlnGlyProLeuAlaProProAlaSerProGlyProPheAlaThrArgSerProLeuPhe 80
Db 347 CAGGCGCGCTGGGCCACCTGCCAGCCTGGCCCTTTTGTCTACAGATCCCGCTTTC 406
Qy 81 IlePheMetArgArgSerSerLeuLeuSerArgSer 92
Db 407 ATCTTTATGAGAAGATCTCTCCCTGCTGTCGATCC 442

RESULT 4
US-09-918-995-36495
; Sequence 36495, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36495
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-36495

Alignment Scores:
Pred. No.: 1.59e-37 Length: 403
Score: 437.00 Matches: 79
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 41.03% Indels: 0
DB: 10 Gaps: 0

US-09-508-832-10 (1-198) x US-09-918-995-36495 (1-403)

Qy 1 MetAlaYsGlnProSerAspValSerSerGluCyAspArgGluGlyArgGlnLeuGln 20
Db 167 ATGCCAAAGCAACCTTCTGATGAAGTCTCAGTGTGACCGAGAGGAGGTAGACAATTGCAG 226
Qy 21 ProAlaGluArgProProGlnLeuArgProGlyAlaProThrSerLeuGlnThrGluPro 40
Db 227 CCTCGGAGAGGCGCTCCACAGCTCAGACCTGGGGCCCTTACTCTCCCTACACAGAGCCA 286
Qy 41 GlnGlyAenProGluGlyAsnHisGlyGlyGluGlyAspSerCysProHisGlySerPro 60
Db 287 CAAGGTAACTCTGAAGCAATACGGAGGTGAGGGGACAGCTGCCCGCCAGCGCCTT 346

Alignment Scores:
Pred. No.: 4.26e-11 Length: 455
Score: 192.00 Matches: 37
Percent Similarity: 90.70% Conservative: 2
Best Local Similarity: 86.05% Mismatches: 4
Query Match: 18.03% Indels: 0
DB: 14 Gaps: 0

US-09-508-832-10 (1-198) x US-10-027-632-75254 (1-455)

Qy 127 TyrLeuSerAlaMetAlaSerMetArgGlnAlaGluProAlaAspMetArgProGluLeu 146
Db 64 TTTTGTCTGTGATGCAGCTTCCATGAGGCGAGGCTGAACCTGCAGATATCGGCCAGAGATA 123
Qy 147 TrpIleAlaGlnGluLeuArgArgIleGlyAspGluPheAsnAlaTyrTyrAlaArgArg 166
Db 124 TGGATCCTCCCAAGAGTTGCGCGGTATYGGAGACAGGTTTAACGCTTACTATGCAAGGAGG 183
Qy 167 ValPheLeu 169
Db 184 GTAATGATG 192

RESULT 6
US-10-027-632-313542
; Sequence 313542, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
```

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US-10-027-632-75254
Alignment Scores:
Pred. No.: 4.26e-11 Length: 455
Score: 192.00 Matches: 37
Percent Similarity: 90.70% Conservative: 2
Best Local Similarity: 86.05% Mismatches: 4
Query Match: 18.03% Indels: 0
DB: 18 Gaps: 0

US-09-508-832-10 (1-198) x US-10-027-632-75254 (1-455)
Qy 127 TyrLeuSerAlaMetAlaSerMetArgGlnAlaGluProAlaAspMetArgProGluIle 146
Db 64 TTTTGTCTGATGCAGCTTCCATGAGGCGGCTGAACCTGCAGATATGCCCCAGAGATA 123
Qy 147 TrpIleAlaGlnGluLeuArgArgIleGlyAspGluPheAsnAlaTyrTyrAlaArgArg 166
Db 124 TGGATCGCCCAAGAGTTGGCGGTATYGGAGACGAGCTTTAAACGCTTACTATGCAAGGAGG 183
Qy 167 ValPheLeu 169
Db 184 GTAATGATG 192

RESULT 8
US-10-027-632-313542
; Sequence 313542, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; TITLE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313542
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-313542
Alignment Scores:
Pred. No.: 4.26e-11 Length: 455
Score: 192.00 Matches: 37
Percent Similarity: 90.70% Conservative: 2
Best Local Similarity: 86.05% Mismatches: 4
Query Match: 18.03% Indels: 0
DB: 18 Gaps: 0

US-09-508-832-10 (1-198) x US-10-027-632-313542 (1-455)
Qy 127 TyrLeuSerAlaMetAlaSerMetArgGlnAlaGluProAlaAspMetArgProGluIle 146
Db 64 TTTTGTCTGATGCAGCTTCCATGAGGCGGCTGAACCTGCAGATATGCCCCAGAGATA 123
Qy 147 TrpIleAlaGlnGluLeuArgArgIleGlyAspGluPheAsnAlaTyrTyrAlaArgArg 166
Db 124 TGGATCGCCCAAGAGTTGGCGGTATYGGAGACGAGCTTTAAACGCTTACTATGCAAGGAGG 183
Qy 167 ValPheLeu 169
Db 184 GTAATGATG 192

RESULT 7
US-10-027-632-75254
; Sequence 75254, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; TITLE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75254
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Human

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US-10-027-632-75254
Alignment Scores:
Pred. No.: 4.26e-11 Length: 455
Score: 192.00 Matches: 37
Percent Similarity: 90.70% Conservative: 2
Best Local Similarity: 86.05% Mismatches: 4
Query Match: 18.03% Indels: 0
DB: 18 Gaps: 0

US-09-508-832-10 (1-198) x US-10-027-632-75254 (1-455)
Qy 127 TyrLeuSerAlaMetAlaSerMetArgGlnAlaGluProAlaAspMetArgProGluIle 146
Db 64 TTTTGTCTGATGCAGCTTCCATGAGCGAGGCTGAACCTGCAGATATGCCCCAGAGATA 123
Qy 147 TrpIleAlaGlnGluLeuArgArgIleGlyAspGluPheAsnAlaTyrTyrAlaArgArg 166
Db 124 TGGATCGCCCAAGAGTTGGCGGTATYGGAGACGAGCTTTAAACGCTTACTATGCAAGGAGG 183
Qy 167 ValPheLeu 169
Db 184 GTAATGATG 192

RESULT 8
US-10-027-632-313542
; Sequence 313542, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; TITLE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313542
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-313542
Alignment Scores:
Pred. No.: 4.26e-11 Length: 455
Score: 192.00 Matches: 37
Percent Similarity: 90.70% Conservative: 2
Best Local Similarity: 86.05% Mismatches: 4
Query Match: 18.03% Indels: 0
DB: 18 Gaps: 0

US-09-508-832-10 (1-198) x US-10-027-632-313542 (1-455)
Qy 127 TyrLeuSerAlaMetAlaSerMetArgGlnAlaGluProAlaAspMetArgProGluIle 146
Db 64 TTTTGTCTGATGCAGCTTCCATGAGCGAGGCTGAACCTGCAGATATGCCCCAGAGATA 123
Qy 147 TrpIleAlaGlnGluLeuArgArgIleGlyAspGluPheAsnAlaTyrTyrAlaArgArg 166
Db 124 TGGATCGCCCAAGAGTTGGCGGTATYGGAGACGAGCTTTAAACGCTTACTATGCAAGGAGG 183
Qy 167 ValPheLeu 169
Db 184 GTAATGATG 192

RESULT 7
US-10-027-632-75254
; Sequence 75254, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; TITLE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75254
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Human

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Db 124 TGGATCGCCCAAGAGTTGCGGGTATYGGAGACGAGTTTAAACGCTTACTATGCAAGGAGG 183
Qy 167 ValPheLeu 169
Db 184 GTAATGATG 192

RESULT 9
US-10-092-750-72
; Sequence 72, Application US/10092750
; Publication No. US20030032157A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, Philip W.
; APPLICANT: Alpin, Julia
; TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
; FILE REFERENCE: 50036/050002
; CURRENT APPLICATION NUMBER: US/10/092,750
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,526
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 199
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-750-72

Alignment Scores:
Pred. No.: 2,99e-11 Length: 199
Score: 189.50 Matches: 39
Percent Similarity: 81.48% Conservativity: 5
Best Local Similarity: 72.22% Mismatches: 5
Query Match: 17.79% Indels: 5
DB: 15 Gaps: 2

US-09-508-832-10 (1-198) x US-10-092-750-72 (1-199)
Qy 124 PheAenHisTyrLeuSerAlaMetAlaSerMetArgGlnAlaGluProAlaAspMetArg 143
Db 33 TACAATTCTTACTTACACA---ATGGCTTCCATGAGGCGAGGCTGAACCTGCAGATATGCGC 89
Qy 144 ProGluIleTrrPileAlaGlnGluLeuArgGlyGlyAspGluPheAsnAlaTyrTyr 163
Db 90 CCAGAGATATGATCGCCCAAGAGTTGCGGCGTATTGGAGACGAGTTTAAACGCTTACTAT 149
Qy 164 AlaArgArgValPheLeuAsnAsnTyrGlnAlaAlaGluAap 177
Db 150 GCAAGG-----GAGGATTACAAAGACGATGCGAT 179

RESULT 10
US-10-092-750-153
; Sequence 153, Application US/10092750
; Publication No. US20030032157A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, Philip W.
; APPLICANT: Alpin, Julia
; APPLICANT: Wright, Martin C.
; TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
; FILE REFERENCE: 50036/050002
; CURRENT APPLICATION NUMBER: US/10/092,750
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,526
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 153
; LENGTH: 105
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-750-153

Alignment Scores:
Pred. No.: 0.00173 Length: 1101
Score: 125.50 Matches: 55
Percent Similarity: 37.10% Conservativity: 14
Best Local Similarity: 29.57% Mismatches: 67
Query Match: 11.78% Indels: 50
```

```
Pred. No.: 2,43e-10 Length: 105
Score: 178.00 Matches: 34
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.71% Indels: 0
DB: 15 Gaps: 0

US-09-508-832-10 (1-198) x US-10-092-750-153 (1-105)
Qy 132 AlaSerMetArgGlnAlaGluProAlaAspMetArgProGluIleTrrPileAlaGlnGlu 151
Db 1 GCTTCCATGAGGCGAGGCTGAACCTGCAGATATGCGCCGAGATATGATGCCCCAAGAG 60
Qy 152 LeuArgArgIleGlyAspGluPheAsnAlaTyrTyrAlaArg 165
Db 61 TTGCGGCGTATTGGAGACGAGTTTAAACGCTTACTATGCAAGG 102

RESULT 11
US-10-282-122A-7256/c
; Sequence 7256, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7256
; LENGTH: 1101
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-7256

Alignment Scores:
Pred. No.: 0.00173 Length: 1101
Score: 125.50 Matches: 55
Percent Similarity: 37.10% Conservativity: 14
Best Local Similarity: 29.57% Mismatches: 67
Query Match: 11.78% Indels: 50
```



```
Db 133617 CTGTGTCGCCAGCGAGTCAGTCGACTCGGCCAGGTGCGCGCTGAGAGAAAGCTCCCGG 133558
Qy 27 nLeuArgProGlyAlaProThrSer-----LeuGln-ThrGluProGlnG 42
Db 133557 TCTCCGCCCGCGCCGCTCGCTCCGAGCCCGCCACATCCGTTTCCGCCCCAGAGT 133498
Qy 42 lYAsnProGluGlyAsnHisGlyGlyGluGlyAspSerCysProHisGlySerProGlnG 62
Db 133497 CTCAGCCAGCAGCTCAACCGCGCGCTCGCGCCCGCGCCGCCACCGCGCGCGCGGCC 133438
Qy 62 lYProLeuAlaProProAlaSerProGlyProPheAlaThrArgSerProLeuPheLeuP 82
Db 133437 CGCTCCAGCGCGCGCCAGCGCGCGCCCGCGCTGCC-----CTTC 133396
Qy 82 heMetArgSerSerLeuLeuSerArgSerSerGlyTyrPheSerPheAspThrA 102
Db 133395 CTCGCCACGGGCTGCTGTGCTCGTCTCGGTCCCTCTCCGCCCGCTCGCTCACTCT 133336
Qy 102 spArgSerProAlaProMetSerCysAspLysSerThrGlnThrProSerProCysG 122
Db 133335 CTCTCCCTCTTCTCTCAGAGGATGTCGGGCTTCCAGATCAACCTCAACC-----C 133285
Qy 122 lnaAlaPheAsnHisTyrLeuSerAlaMetAlaSerMetArgGlnAlaGluProAlaAspM 142
Db 133284 GCTCAAGGAGCCACTCGGCTTCATCAAGGTCCTCGAGTGGGTGAGTGCAGCGCGCGCGG 133225
Qy 142 etArgProGluLeuTrpIleAlaGlnGluLeuArgArgIleGlyAsp 157
Db 133224 CCAGCGCCGCTCGCGCTCGCGCGCGCGCTTAGCGG---GGAGAC 133181
RESULT 14
US-10-981-277-22/c
; Sequence 22, Application US/10981277
; Publication No. US20050181389A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; TITLE OF INVENTION: Compositions and Methods for Glioma Classification
; FILE REFERENCE: 03-968-US
; CURRENT APPLICATION NUMBER: US/10/981,277
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/516,817
; PRIOR FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 151882
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-981-277-22
Alignment Scores:
Pred. No.: 1.99 Length: 151882
Score: 120.50 Matches: 46
Percent Similarity: 45.22% Conservative: 25
Best Local Similarity: 23.30% Mismatches: 69
Query Match: 11.31% Indels: 17
Gaps: 4
DB: 24
US-09-508-832-10 (1-198) x US-10-981-277-22 (1-151882)
Qy 8 ValSerSerGluCysAspArgGluGlyArg-GlnLeuGlnProAlaGluArgProGln 27
Db 89481 CTGTGTCGCCAGCGGATCAGTCGACTCGGCCAGGTGCGGCTGAGGAGAGCTCCCGG 89422
Qy 27 nLeuArgProGlyAlaProThrSer-----LeuGln-ThrGluProGlnG 42
Db 89421 TCTCCGCCCGCGCGCGCTCGCTCCCGCTCCCGCGCGCGCGCGCTCGCTCGCTCGCTCGCT 89362
Qy 42 lYAsnProGluGlyAsnHisGlyGlyGluGlyAspSerCysProHisGlySerProGlnG 62
Db 89361 CTCAGCCAGCAGCTCAACCGCGCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 89302
```

```
Qy 62 lYProLeuAlaProProAlaSerProGlyProPheAlaThrArgSerProLeuPheLeuP 82
Db 89301 GGCCTCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 89260
Qy 82 heMetArgSerSerLeuLeuSerArgSerSerGlyTyrPheSerPheAspThrA 102
Db 89259 CTCGCCACCGCGGCTGCTGTGCTCGTCTCGTCCCGCTCCCGCGCGCGCGCGCGCT 89200
Qy 102 spArgSerProAlaProMetSerCysAspLysSerThrGlnThrProSerProCysG 122
Db 89199 CTCTCCCTCTTCTCTCAGAGGATGTCGGGCTTCCAGATCAACCTCAACC-----C 89149
Qy 122 lnaAlaPheAsnHisTyrLeuSerAlaMetAlaSerMetArgGlnAlaGluProAlaAspM 142
Db 89148 GCTCAAGGAGCCACTCGGCTTCATCAAGGTCCTCGAGTGGGTGAGTGCAGCGCGCGCGG 89089
Qy 142 etArgProGluLeuTrpIleAlaGlnGluLeuArgArgIleGlyAsp 157
Db 89088 CCAGCGCGCGCTCGCGCTCGCGCGCGCGCGCTTAGCGG---GGAGAC 89045
RESULT 15
US-10-158-160A-14/c
; Sequence 14, Application US/10158160A
; Publication No. US20030059805A1
; GENERAL INFORMATION:
; APPLICANT: RAPPOLD-HOERBRAND, GUDRUN
; TITLE OF INVENTION: HUMAN GROWTH GENE AND SHORT STATURE GENE REGION
; FILE REFERENCE: 108351-00004
; CURRENT APPLICATION NUMBER: US/10/158,160A
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 09/147,699
; PRIOR FILING DATE: 1999-06-24
; PRIOR APPLICATION NUMBER: PCT/EP97/05355
; PRIOR FILING DATE: 1997-09-29
; PRIOR APPLICATION NUMBER: 60/027,633
; PRIOR FILING DATE: 1996-10-01
; PRIOR APPLICATION NUMBER: EP/97100583.0
; PRIOR FILING DATE: 1997-01-16
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 32367
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-158-160A-14
Alignment Scores:
Pred. No.: 0.412 Length: 32367
Score: 119.50 Matches: 60
Percent Similarity: 41.24% Conservative: 13
Best Local Similarity: 33.90% Mismatches: 59
Query Match: 11.22% Indels: 45
Gaps: 11
DB: 15
US-09-508-832-10 (1-198) x US-10-158-160A-14 (1-32367)
Qy 9 SerSerGluCysAspArgGluGlyArg-----GlnLeuGlnProAlaGluArgProPro 26
Db 14144 TCCCAAGCCTCTCCCGGAGACACAGGTCGTCAGGCTTCCCGGGTCACAGGTCCTCCCA 14085
Qy 27 GlnLeu-----ArgProGlyAlaProThrSerLeuGln---Thr-GluProGlnGln 42
Db 14084 AGGCTCTCTCCGAGACACAGGTCCTCCCGAGGACACAGGTCCTCCCGAGGATCCCAAGG 14025
Qy 42 lYAsnProGlu-----GlyAsnHisGlyGlyGln 51
Db 14024 CTCTCCAGGACACACAGGTCCTCCCGAGGACACAGGTCCTCCCGAGGATCCCAAGGTCCT 13965
Qy 51 uGlyAspSerCysProHisGlySerProGln-----GlyProLeuAlaProAlaSe 69
Db 13964 CGGGTCTACTAGGTCTCCCAAGGACATCCCGAGACACACAGGTCCTCCCAAGGCTCTCC 13905
```

```
QY 69 rProGlyProPheAla-----ThrArgSerProLeuPheIlePheMetArgAr 85
Db 13904 ACCAGGTCCCAAGGCTCTCCCAAGGACACCAAGGTCTCCCGGTCAACAG 13845
QY 85 gSerSerLeuLeuSerArg---SerSerSerGlyTyrPheSerPheAspThr----- 101
Db 13844 GTCCCAAGGCTCTCCAGGTCAACCAAGGTCTCCCAAGGCTCTCTGGGACACCAAGGTTC 13785
QY 102 -----AspArg-SerProAlaProMetSerCysAspLysSerThrGlnThrPro----- 117
Db 13784 AAGCCTCTCCCGGACACCAAGTCCCAAGCC-----TCTCCCGGACACCAAGGTTC 13734
QY 118 -----SerProCysGlnAlaPheAsnHisTyrLeuSerAlaMetA 132
Db 13733 CCCAAGCCTCTCCCGCTCACCAGATCTCCAAGCCTCTCCCAAGGACACCAAGGTCCCAAG 13674
QY 132 laSerMetArg-----GlnAlaGluProAlaAspMetArg 143
Db 13673 CCTCTCCCAAGGACACCAAGGTCCCAAGCCTCTCTCCCAAGGACACCAAGG 13627
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Search completed: November 12, 2005, 08:27:46
Job time : 849 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2005, 04:59:33 ; Search time 28 Seconds
(without alignments)
527.876 Million cell updates/sec

Title: US-09-508-832-10

Perfect score: 1065

Sequence: 1 MAKQPSDVSSCDREGROLQ.....PRMVLRLRYVRLVWRMH 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	696	65.4	138	4	US-09-949-016-11305
2	144	13.5	27	4	US-09-544-664B-19
3	114	10.7	160	4	US-09-252-991A-27091
4	111.5	10.5	886	2	US-08-474-379C-65
5	111.5	10.5	886	3	US-09-146-249A-65
6	111.5	10.5	886	3	US-08-206-188B-65
7	111.5	10.5	901	4	US-09-917-254-93
8	108.5	10.2	885	2	US-08-577-492-33
9	108.5	10.2	885	3	US-09-079-630-33
10	103	9.7	1706	4	US-09-252-991A-31760
11	100	9.4	607	4	US-09-949-016-7817
12	100	9.4	627	4	US-08-487-596-6
13	100	9.4	627	4	US-08-660-451A-6
14	99	9.3	228	3	US-09-219-849-38
15	99	9.3	375	4	US-09-600-932-29
16	99	9.3	1057	3	US-08-931-820-4
17	99	9.3	1078	3	US-08-963-825-21
18	99	9.3	1078	3	US-09-500-811-21
19	99	9.3	1078	3	US-09-570-573-21
20	99	9.3	1078	3	US-09-548-608-21
21	98	9.2	349	4	US-09-252-991A-29455
22	97.5	9.2	1505	4	US-09-538-092-1102
23	97	9.1	372	4	US-09-252-991A-32717
24	95.5	9.0	50	4	US-09-621-976-5959
25	95	8.9	1516	4	US-09-949-016-8209
26	94.5	8.9	132	4	US-09-489-039A-9920
27	94.5	8.9	280	3	US-09-247-155-178

28	94.5	8.9	684	4	US-09-961-403-5	Sequence 5, Appli
29	94.5	8.9	1184	4	US-09-266-225D-18	Sequence 18, Appli
30	94.5	8.9	1185	3	US-09-041-886-23	Sequence 23, Appli
31	94.5	8.9	1185	4	US-09-538-032-1209	Sequence 1209, Ap
32	94	8.8	322	4	US-09-949-016-8332	Sequence 8332, Ap
33	94	8.8	562	4	US-09-879-752-12	Sequence 12, Appli
34	94	8.8	580	3	US-08-906-865-1	Sequence 1, Appli
35	94	8.8	580	4	US-09-129-668-1	Sequence 1, Appli
36	94	8.8	627	2	US-08-466-589-6	Sequence 6, Appli
37	94	8.8	627	2	US-08-700-636-6	Sequence 6, Appli
38	94	8.8	627	3	US-08-467-574-6	Sequence 6, Appli
39	94	8.8	627	3	US-09-217-345-6	Sequence 6, Appli
40	94	8.8	627	4	US-09-892-985-6	Sequence 6, Appli
41	93.5	8.8	245	4	US-09-311-021-104	Sequence 104, App
42	93.5	8.8	434	2	US-08-710-249-4	Sequence 4, Appli
43	93.5	8.8	434	3	US-09-220-157A-4	Sequence 4, Appli
44	93.5	8.8	902	1	US-08-396-479B-6	Sequence 6, Appli
45	93.5	8.8	902	1	US-08-818-823-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-949-016-11305
; Sequence 11305, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11305
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-11305

Query Match	65.4%	Score 696;	DB 4;	Length 138;
Best Local Similarity	69.7%	Pred. No. 1.7e-63;		
Matches 138;	Conservative	0;	Mismatches 0;	Indels 60; Gaps 1;
QY	1	MAKQPSDVSSCDREGROLQPAERPPOLRPGAPTSLQTEPQGNPEGNHGGEDSCPHGSP	60	
DB	1	MAKQPSDVSSCDREGROLQPAERPPOLRPGAPTSLQTEPQ	41	
QY	61	QGLAPPASPGPFATRSPLIFMRSSLLSSSGYFSFDTDRSPAPMSCDKSTQTPSP	120	
DB	42	-----DRSPAPMSCDKSTQTPSP	60	
QY	121	COAFNHYLSAMASMRQAEPAEMRPEIWTAEQLRIGDEFNAYARRVFLNNYQAAEDHPR	180	
DB	61	COAFNHYLSAMASMRQAEPAEMRPEIWTAEQLRIGDEFNAYARRVFLNNYQAAEDHPR	120	
QY	181	MVILRLRYVRLVWRMH	198	
DB	121	MVILRLRYVRLVWRMH	138	

RESULT 2

US-09-544-664B-19
; Sequence 19, Application US/09544664B
; Patent No. 6713280

GENERAL INFORMATION:
APPLICANT: Huang, Ziwei
APPLICANT: Wang, Jialun
APPLICANT: Zhang, Zhijia
APPLICANT: Shan, Simei
APPLICANT: Lu, Zhixian
TITLE OF INVENTION: Enhancement of Peptide Cellular Uptake
FILE REFERENCE: 8321-66
CURRENT APPLICATION NUMBER: US/09/544,664B
CURRENT FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: PCT/US00/09352
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/128,202
PRIOR FILING DATE: 1999-04-07
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 27
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide
OTHER INFORMATION: segment from BH3 domain of a Bcl-2 superfamily
OTHER INFORMATION: polypeptide
US-09-544-664B-19

Query Match 13.5%; Score 144; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 DMRPEIWTIAQLRRIGDGFENYARRV 167
DB 1 DMRPEIWTIAQLRRIGDGFENYARRV 27

RESULT 3
US-09-252-991A-27091
Sequence 27091, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27091
LENGTH: 160
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27091

Query Match 10.7%; Score 114; DB 4; Length 160;
Best Local Similarity 30.6%; Pred. No. 0.00065;
Matches 44; Conservative 10; Mismatches 56; Indels 34; Gaps 7;

QY 21 PAERPPQLRGG---APTSLQTEPQ-----NPEGNH-----GGGDCSCPHGSPQGPLAPPAS 69
DB 18 PRKKPPARPQPCAPGRLPSPRPGGAAGNAPPGRGSSATPGSGGAPPAPPAR 77
QY 70 PGPFATRSPLFIEMRRSSLLSRSSSGYFSDTD-RSPAPMS-----CDKSTQTPSP 119
DB 78 RARRAGRDD-----GRSAATAR-----DRDSRSPAPRGAGRARSRCRRPGRPPR 124
QY 120 PCQAFNHYLSAMASMRQAEPADMR 143
DB 125 PASASADRLARVATRHAGRPVGR 148

GENERAL INFORMATION:
APPLICANT: Huang, Ziwei
APPLICANT: Wang, Jialun
APPLICANT: Zhang, Zhijia
APPLICANT: Shan, Simei
APPLICANT: Lu, Zhixian
TITLE OF INVENTION: Enhancement of Peptide Cellular Uptake
FILE REFERENCE: 8321-66
CURRENT APPLICATION NUMBER: US/09/544,664B
CURRENT FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: PCT/US00/09352
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/128,202
PRIOR FILING DATE: 1999-04-07
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 27
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide
OTHER INFORMATION: segment from BH3 domain of a Bcl-2 superfamily
OTHER INFORMATION: polypeptide
US-09-544-664B-19

Query Match 13.5%; Score 144; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 DMRPEIWTIAQLRRIGDGFENYARRV 167
DB 1 DMRPEIWTIAQLRRIGDGFENYARRV 27

RESULT 3
US-09-252-991A-27091
Sequence 27091, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27091
LENGTH: 160
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27091

Query Match 10.7%; Score 114; DB 4; Length 160;
Best Local Similarity 30.6%; Pred. No. 0.00065;
Matches 44; Conservative 10; Mismatches 56; Indels 34; Gaps 7;

QY 21 PAERPPQLRGG---APTSLQTEPQ-----NPEGNH-----GGGDCSCPHGSPQGPLAPPAS 69
DB 18 PRKKPPARPQPCAPGRLPSPRPGGAAGNAPPGRGSSATPGSGGAPPAPPAR 77
QY 70 PGPFATRSPLFIEMRRSSLLSRSSSGYFSDTD-RSPAPMS-----CDKSTQTPSP 119
DB 78 RARRAGRDD-----GRSAATAR-----DRDSRSPAPRGAGRARSRCRRPGRPPR 124
QY 120 PCQAFNHYLSAMASMRQAEPADMR 143
DB 125 PASASADRLARVATRHAGRPVGR 148

RESULT 4
US-08-474-379C-65
Sequence 65, Application US/08474379C
Patent No. 5977305
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
TITLE OF INVENTION: PROCESSES
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,379C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/206,188
FILING DATE: 01-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,352
FILING DATE: 19-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 27866/32771
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 886 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-379C-65

Query Match 10.5%; Score 111.5; DB 2; Length 886;
Best Local Similarity 27.5%; Pred. No. 0.011;
Matches 47; Conservative 18; Mismatches 67; Indels 39; Gaps 7;

QY 6 SDVSSCEDRGRLQLOPAERPPOL-----RPGATSLQTEPQ-----GNPGRNHGG-----50
DB 49 SOSAERAEERQPHRIERADADMTSDRPLRTTMSWSPSHGTGTGSGGAGGSSRRF 108
QY 51 EGDSCPHGSP-QGPLAPPASPGFFATRSPLFIEMRRSSLLSRSSSGYFSDTDSPAPMS 109
DB 109 EAENGTPSPGRSPLDSQASPG-LVLHAGAATSQRRESFLYRSDSY-----DMSPKTWS 162
QY 110 CDKSTQTPSPPCQAFNHYLSAMASMRQAEPADMRPEIWTIAQLRRIGDGFEN 160
DB 163 RN-----SSVTSEAHAEEDLIVTPPAQVLASLRSVRSNFS 196

RESULT 5
US-09-146-249A-65
Sequence 65, Application US/09146249A
Patent No. 6069240
GENERAL INFORMATION:

APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,249A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 886 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-146-249A-65

Query Match 10.5%; Score 111.5; DB 3; Length 886;
Best Local Similarity 27.5%; Pred. No. 0.011; Mismatches 18; Indels 39; Gaps 7;
Matches 47; Conservative 18; Mismatches 67; Indels 39; Gaps 7;
QY 6 SDVSSECDREGRLQQAERPPQL-----RPGAPTSIQTEPQ-----GNPEGNHGG----- 50
DB 49 SDSAERAERQPHRPIERADAMDTSDRGLTTRMSWPSFHGTTGSGGAGGSSRRF 108
QY 51 EGDSCPHGSP-QGPLAPPSPGPFATRSPLFIFMRSSLLRSGSGYFSFTDRSPAPMS 109
DB 109 EAENGTPSPGRSPLDSQSPG-LVLHAGAATSQRRSFYRSDSDY-----DMSPKTMS 162
QY 110 CDKSTQTSPPCQAFNHYLSAMSRQAEPMRPEIWIQAELRRIGDEFN 160
DB 163 RN-----SSVTSEAHEDLIVTPFAQVLASLRVSRNFS 196

RESULT 6
US-08-206-188B-65
Sequence 65, Application US/08206188B
Patent No. 6100025
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,188B
FILING DATE: 01-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 886 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-206-188B-65

Query Match 10.5%; Score 111.5; DB 3; Length 886;
Best Local Similarity 27.5%; Pred. No. 0.011; Mismatches 18; Indels 39; Gaps 7;
Matches 47; Conservative 18; Mismatches 67; Indels 39; Gaps 7;
QY 6 SDVSSECDREGRLQQAERPPQL-----RPGAPTSIQTEPQ-----GNPEGNHGG----- 50
DB 49 SDSAERAERQPHRPIERADAMDTSDRGLTTRMSWPSFHGTTGSGGAGGSSRRF 108
QY 51 EGDSCPHGSP-QGPLAPPSPGPFATRSPLFIFMRSSLLRSGSGYFSFTDRSPAPMS 109
DB 109 EAENGTPSPGRSPLDSQSPG-LVLHAGAATSQRRSFYRSDSDY-----DMSPKTMS 162
QY 110 CDKSTQTSPPCQAFNHYLSAMSRQAEPMRPEIWIQAELRRIGDEFN 160
DB 163 RN-----SSVTSEAHEDLIVTPFAQVLASLRVSRNFS 196

RESULT 7
US-09-917-254-93
Sequence 93, Application US/09917254
Patent No. 6703204
GENERAL INFORMATION:
APPLICANT: Mutter, George
APPLICANT: Baak, Jan
TITLE OF INVENTION: Prognostic Classification of Breast Cancer
FILE REFERENCE: B0801/724(JRV)
CURRENT APPLICATION NUMBER: US/09/917,254
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: US 60/222,093
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
SEQ ID NO 93
LENGTH: 901
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-917-254-93

Query Match 10.5%; Score 111.5; DB 4; Length 901;
Best Local Similarity 27.5%; Pred. No. 0.011; Mismatches 18; Indels 39; Gaps 7;
Matches 47; Conservative 18; Mismatches 67; Indels 39; Gaps 7;
QY 6 SDVSSECDREGRLQQAERPPQL-----RPGAPTSIQTEPQ-----GNPEGNHGG----- 50
DB 64 SDSAERAERQPHRPIERADAMDTSDRGLTTRMSWPSFHGTTGSGGAGGSSRRF 123

Query Match 10.5%; Score 111.5; DB 4; Length 901;
Best Local Similarity 27.5%; Pred. No. 0.011; Mismatches 18; Indels 39; Gaps 7;
Matches 47; Conservative 18; Mismatches 67; Indels 39; Gaps 7;
QY 6 SDVSSECDREGRLQQAERPPQL-----RPGAPTSIQTEPQ-----GNPEGNHGG----- 50
DB 64 SDSAERAERQPHRPIERADAMDTSDRGLTTRMSWPSFHGTTGSGGAGGSSRRF 123

;; CURRENT APPLICATION NUMBER: US/09/252,991A
;; CURRENT FILING DATE: 1999-02-18
;; PRIOR APPLICATION NUMBER: US 60/074,788
;; PRIOR FILING DATE: 1998-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,190
;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 31760
;; LENGTH: 1706
;; TYPE: PRT
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31760

Query Match 9.4%; Score 103; DB 4; Length 1706;
Best Local Similarity 29.7%; Pred. No. 0.19;
Matches 52; Conservative 17; Mismatches 56; Indels 50; Gaps 13;
QY 2 AKQPSDVSECDREGRLQPAERPP-QLRPGAPTSLOTPEQGNPEGNHGGEGDS---CPH 57
DB 435 ARPPAALPARA-RRGRRQPPGRPRRLRPGAPVAAAPATGG-AATFPGAGDSRHRCS 492
QY 58 GS-----PQGPLA-----PPASPGPFATR-----SPLFIMRRSSLLSRSSSGYFSFDT 101
DB 493 GTDRCPRPQPAARDPGSGWFGSAARRAARGDP-----HRRETAL-RSAA----- 540
QY 102 DRSPAPMSCDKSTQTFSPPCQAFNHYLSAMASMQA-----EPADMRP 144
DB 541 -RRPR-READPPGRTPAQPGQ--TEGARRLARRRTAGTAAPHRHRQPPQAPGRP 591

RESULT 11
US-09-949-016-7817
;; Sequence 7817, Application US/09949016
;; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: CL001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 7817
;; LENGTH: 607
;; TYPE: PRT
;; ORGANISM: Human
US-09-949-016-7817

Query Match 9.4%; Score 100; DB 4; Length 607;
Best Local Similarity 26.4%; Pred. No. 0.099;
Matches 33; Conservative 15; Mismatches 43; Indels 34; Gaps 5;
QY 1 MAKQPSDVSECDREGRLQPAERPPQLRPGAPTSLOTPEQGNPEGNHGGEGDSCTPHGSP 60
DB 337 LMKRPSVVKDNCRRLLIESMHKMASAPREW-----EPEGPATSGTQSLHPPSPSF 388
QY 61 QGPLAPPASPGPFATRSPLFIMRRSSLLSRSSSGYFSFDTDRSP--APMSCDKSTQTPS 118
DB 389 CVPILDVPAEPGP-SCKSP-----SDQLPPQPPLEAKASPHPS 425
QY 119 P-PCQ 122
DB 426 PGPCR 430

RESULT 12

US-08-487-596-6
;; Sequence 6, Application US/08487596
;; Patent No. 6440681
;; GENERAL INFORMATION:
;; APPLICANT: Elliot, Kathryn J.
;; APPLICANT: Ellis, Steven B.
;; APPLICANT: Harpold, Michael M.
;; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
;; ANTAGONISTS FOR HUMAN NEURONAL
;; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
;; NUMBER OF SEQUENCES: 18
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Brown, Martin, Haller & McClain
;; STREET: 1660 Union Street
;; CITY: San Diego
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 92101
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA: US/08/487,596
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO US94/02447
;; FILING DATE: 08-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/149,503
;; FILING DATE: 08-NOV-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/028,031
;; FILING DATE: 08-MAR-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/938,154
;; FILING DATE: 30-NOV-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/504,455
;; FILING DATE: 03-APR-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Seidman, Stephanie L.
;; REGISTRATION NUMBER: 33,779
;; REFERENCE/DOCKET NUMBER: 6362-9951
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-238-0999
;; TELEFAX: 619-238-0062
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 627 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
US-08-487-596-6

Query Match 9.4%; Score 100; DB 4; Length 627;
Best Local Similarity 26.4%; Pred. No. 0.1;
Matches 33; Conservative 15; Mismatches 43; Indels 34; Gaps 5;
QY 1 MAKQPSDVSECDREGRLQPAERPPQLRPGAPTSLOTPEQGNPEGNHGGEGDSCTPHGSP 60
DB 357 LMKRPSVVKDNCRRLLIESMHKMASAPREW-----EPEGPATSGTQSLHPPSPSF 408
QY 61 QGPLAPPASPGPFATRSPLFIMRRSSLLSRSSSGYFSFDTDRSP--APMSCDKSTQTPS 118
DB 409 CVPILDVPAEPGP-SCKSP-----SDQLPPQPPLEAKASPHPS 445
QY 119 P-PCQ 122
DB 446 PGPCR 450

RESULT 13
US-08-660-451A-6
; Sequence 6, Application US/08660451A
; Patent No. 6524789
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,451A
; FILING DATE: June 7, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,722
; FILING DATE: 06/07/95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9370B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-660-451A-6

Query Match 9.4%; Score 100; DB 4; Length 627;
Best Local Similarity 26.4%; Pred. No. 0.1;
Matches 33; Conservative 15; Mismatches 43; Indels 34; Gaps 5;
QY 1 MAKQPSDVSECDREGRLQPAERPPQLRPGAPTSLSQTEPQGNPEGHGGDSCPHGSP 60
DB 357 LMKRPSVVKNDCKRLLESMMKASAPRFPW-----EPGEPPATSGTSLHPPSPGF 408
QY 61 CQPLAPPAGPFPATRSPLFIEMRRSSLLSRSSGYFSDTRSP--APMSCDKSTQTPS 118
DB 409 CVPLDVPAPFGP-SCKSP-----SDQLPQQPLEAKASPHFS 445
QY 119 P-PCQ 122
DB 446 PGPCR 450

RESULT 14
US-09-219-849-38
; Sequence 38, Application US/09219849
; Patent No. 6150081
; GENERAL INFORMATION:

; APPLICANT: VAN HEERDE, GEORGE V.
; APPLICANT: VAN RIJN, ALEXIS C.
; APPLICANT: BOUNSTRA, JAN B.
; APPLICANT: DE WOLF, FREDERIK A.
; APPLICANT: MOOBROEK, ANDREAS
; APPLICANT: WERTEN, MARC W.T.
; APPLICANT: WIND, RICHEL D.
; APPLICANT: VAN DEN BOSCH, TANJA J.
; TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
; TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
; TITLE OF INVENTION: PREPARATION THEREOF
; FILE REFERENCE: 2728-2
; CURRENT APPLICATION NUMBER: US/09/219,849
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: amino acid sequence
US-09-219-849-38

Query Match 9.3%; Score 99; DB 3; Length 228;
Best Local Similarity 35.4%; Pred. No. 0.035;
Matches 29; Conservative 8; Mismatches 31; Indels 14; Gaps 4;
QY 5 PSDVSSECDREGRLQPAER---PPQLRPGAP-TSLQTEPQGNP-----EGNHGGRG 52
DB 66 PQIKGESGKPGASCHNGERPPGPGQLPGQPGTAGPGRDNGPSDQPGRDGSPGKG 125
QY 53 DSCPHGSPQGLAP--PASPGP 72
DB 126 DRGENSGPAGPAGHPGPGP 147

RESULT 15
US-09-600-932-29
; Sequence 29, Application US/09600932
; Patent No. 6787639
; GENERAL INFORMATION:
; APPLICANT: Wakamiya, No. 6787639utaka
; TITLE OF INVENTION: NOVEL COLLECTIN
; FILE REFERENCE: 19036/36615
; CURRENT APPLICATION NUMBER: US/09/600,932
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: PCT/JP98/03328
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: JP 10-11281
; PRIOR FILING DATE: 1998-01-23
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: surfactant protein D (SP-D)
US-09-600-932-29

Query Match 9.3%; Score 99; DB 4; Length 375;
Best Local Similarity 34.7%; Pred. No. 0.067;
Matches 26; Conservative 8; Mismatches 31; Indels 10; Gaps 3;
QY 14 REGRLQPAERPPQLRPGAPTSLS-----QTEPQGNPEGHGGDSCPHG--SPQGPL 64
DB 50 RDGRDREGPRKEKGDGGLPGAGQAGMPQAGPVG-PKGDNGSVGEPGPKGDTGSPGP 108
QY 65 APPASGPPFATRSPL 79
DB 109 GPGVPGPAGREGPL 123

Search completed: November 12, 2005, 06:38:50
Job time : 30 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 12, 2005, 06:25:58 ; Search time 80 Seconds
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1035.563 Million cell updates/sec

Title: US-09-508-832-10
Perfect score: 1065
Sequence: 1 MAKQPSVSSCDREGROLQ.....PRMVLRLRYIVRLVWRMH 198

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Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	696	65.4	138	14	US-10-092-750-241
2	696	65.4	138	16	US-10-755-889-16
3	497	46.7	92	18	US-10-450-783-31522
4	194	18.2	64	9	US-09-971-980-62
5	194	18.2	64	18	US-10-966-576-62
6	178	16.7	35	14	US-10-092-750-1
7	164	15.4	50	9	US-09-971-980-64
8	164	15.4	50	18	US-10-966-576-64
9	114	10.7	949	16	US-10-437-963-192001
10	111.5	10.5	410	16	US-10-437-963-196665
11	111.5	10.5	886	15	US-10-332-065-2

12	111.5	10.5	886	16	US-10-408-765A-261	Sequence 261, App
13	111.5	10.5	901	18	US-10-450-763-37429	Sequence 37429, A
14	111.5	10.5	1029	14	US-10-257-909A-24	Sequence 24, Appl
15	111.5	10.5	1124	14	US-10-257-909A-6	Sequence 6, Appl
16	111.5	10.5	1132	14	US-10-257-909A-4	Sequence 4, Appl
17	111.5	10.5	1132	14	US-10-257-909A-8	Sequence 8, Appl
18	111.5	10.5	1132	14	US-10-257-909A-32	Sequence 32, Appl
19	111.5	10.4	531	18	US-10-450-763-51899	Sequence 51899, A
20	110	10.3	1764	16	US-10-437-963-192101	Sequence 192101,
21	109	10.2	1680	16	US-10-437-963-192175	Sequence 192175,
22	108	10.1	1851	16	US-10-437-963-192171	Sequence 192171,
23	107	10.0	1694	16	US-10-437-963-192057	Sequence 192057,
24	106.5	10.0	783	14	US-10-241-220-93	Sequence 93, Appl
25	106.5	10.0	783	14	US-10-301-822-59	Sequence 59, Appl
26	106.5	10.0	783	15	US-10-295-027-1191	Sequence 1191, Ap
27	106.5	10.0	783	16	US-10-872-972-93	Sequence 93, Appl
28	106.5	10.0	783	16	US-10-872-991-93	Sequence 93, Appl
29	106.5	10.0	783	17	US-10-916-064-6	Sequence 6, Appl
30	106.5	10.0	783	18	US-10-756-149-5686	Sequence 5686, Ap
31	106.5	10.0	783	18	US-10-983-340-10	Sequence 10, Appl
32	106.5	10.0	950	20	US-11-097-143-41331	Sequence 41331, A
33	106	10.0	20	16	US-10-658-028A-2	Sequence 2, Appl
34	106	10.0	810	14	US-10-156-761-10081	Sequence 10081, A
35	106	10.0	1347	16	US-10-437-963-191996	Sequence 191996,
36	106	10.0	1416	16	US-10-437-963-192143	Sequence 192143,
37	106	10.0	1487	16	US-10-437-963-188109	Sequence 188109,
38	106	10.0	1848	16	US-10-437-963-192129	Sequence 192129,
39	105.5	9.9	574	14	US-10-168-097A-76	Sequence 76, Appl
40	105.5	9.9	574	14	US-10-239-431A-38	Sequence 38, Appl
41	104.5	9.8	706	15	US-10-424-599-218604	Sequence 218604,
42	104	9.8	1504	15	US-10-374-780A-1457	Sequence 1457, Ap
43	104	9.8	1504	16	US-10-437-963-192134	Sequence 192134,
44	104	9.8	1851	16	US-10-437-963-192177	Sequence 192177,
45	103.5	9.7	248	16	US-10-425-115-208167	Sequence 208167,

ALIGNMENTS

RESULT 1
US-10-092-750-241
; Sequence 241, Application US/10092750
; Publication No. US20030032157A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, Philip W.
; APPLICANT: Alpin, Julia
; APPLICANT: Wright, Martin C.
; TITLE OF INVENTION: Polypeptides Interactive with BCL-XI
; FILE REFERENCE: 50036/050002
; CURRENT APPLICATION NUMBER: US/10/092,750
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,526
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 241
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-750-241

Query Match 65.4%; Score 696; DB 14; Length 138;
Best Local Similarity 69.7%; Pred. No. 1.2e-50;
Matches 138; Conservative 0; Mismatches 0; Indels 60; Gaps 1;
QY 1 MAKQPSVSSCDREGROLQPAERPQLRPGAPTSLOTEPQGNPGNHGEGSDSCPHGSP 60
DB 1 MAKQPSVSSCDREGROLQPAERPQLRPGAPTSLOTEPQGNPGNHGEGSDSCPHGSP 41
QY 61 QGLAPPASPGPFATRSPLFIEMRSSLSRSSGVFSFDTDRSPAPMSCDKSTOTPSPP 120
DB 42 -----DRSPAPMSCDKSTOTPSPP 60

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QY 121 COAFNHYLSAMSMRQAEADMRPEIWIQAELRRIGDEFNAYYARRVFLNNYQAEDHPR 180
DB 61 COAFNHYLSAMSMRQAEADMRPEIWIQAELRRIGDEFNAYYARRVFLNNYQAEDHPR 120

QY 181 MVILRLRYIVRLVWRMH 198
DB 121 MVILRLRYIVRLVWRMH 138

RESULT 2
US-10-755-889-16
; Sequence 16, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-16

Query Match 65.4%; Score 696; DB 16; Length 138;
Best Local Similarity 69.7%; Pred. No. 1.2e-50;
Matches 138; Conservative 0; Mismatches 0; Indels 60; Gaps 1;

QY 1 MAKQPSDVSSCDREGROLQPAERPPQLRPGAPTSIQTEPQGNPEGNHGEGDSCPHGSP 60
DB 1 MAKQPSDVSSCDREGROLQPAERPPQLRPGAPTSIQTEPQ----- 41

QY 61 QGPLAPPASPGPFATRSPLFIEMRSSLSRSSGYSFDTDRSPAPMSCDKSTQTPSP 120
DB 42 -----DRSPAPMSCDKSTQTPSP 60

QY 121 COAFNHYLSAMSMRQAEADMRPEIWIQAELRRIGDEFNAYYARRVFLNNYQAEDHPR 180
DB 61 COAFNHYLSAMSMRQAEADMRPEIWIQAELRRIGDEFNAYYARRVFLNNYQAEDHPR 120

QY 181 MVILRLRYIVRLVWRMH 198
DB 121 MVILRLRYIVRLVWRMH 138

RESULT 3
US-10-450-763-31522
; Sequence 31522, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 31522
; LENGTH: 92
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-31522

Query Match 46.7%; Score 497; DB 18; Length 92;
Best Local Similarity 100.0%; Pred. No. 4e-34;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKQPSDVSSCDREGROLQPAERPPQLRPGAPTSIQTEPQGNPEGNHGEGDSCPHGSP 60
DB 1 MAKQPSDVSSCDREGROLQPAERPPQLRPGAPTSIQTEPQGNPEGNHGEGDSCPHGSP 60

QY 61 QGPLAPPASPGPFATRSPLFIEMRSSLSRS 92
DB 61 QGPLAPPASPGPFATRSPLFIEMRSSLSRS 92

RESULT 4
US-09-971-980-62
; Sequence 62, Application US/09971980
; Patent No. US20020164349A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, David B.
; TITLE OF INVENTION: Compositions and Methods of Using Capsid Protein From Flaviviruses
; FILE REFERENCE: Upn-4105
; CURRENT APPLICATION NUMBER: US/09/971,980
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/237,885
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020164349A1el Sequence
US-09-971-980-62

Query Match 18.2%; Score 194; DB 9; Length 64;
Best Local Similarity 68.8%; Pred. No. 7.2e-09;
Matches 44; Conservative 8; Mismatches 8; Indels 4; Gaps 3;

QY 132 ASMRQA--EPADMRPEIWIQAELRRIGDEFNAYYARRVFLNNYQAEDHPRMVILRLRY 189
DB 3 ASIRQSQEPEDLRPEIRI-QELRRIGDEFNETYTRRVFA-DYREAEDHPQMVILQLLRF 60

QY 190 IVRL 193
DB 61 IPRL 64

RESULT 5
US-10-966-576-62
; Sequence 62, Application US/10966576
; Publication No. US20050226849A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, David B.
; TITLE OF INVENTION: Compositions and Methods of Using Capsid Protein From Flaviviruses
; FILE REFERENCE: Upn-4105
; CURRENT APPLICATION NUMBER: US/10/966,576
; CURRENT FILING DATE: 2004-10-14
; PRIOR APPLICATION NUMBER: US/09/971,980
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/237,885
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
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RESULT 7
US-09-971-980-64
; Sequence 64, Application US/09971980
; Patent No. US20020164349A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, David B.
; APPLICANT: Yang, Joo-Sung
; TITLE OF INVENTION: Compositions and Meth-
; TITLE OF INVENTION: Festiviruses
; FILE REFERENCE: Upn-4105
; CURRENT APPLICATION NUMBER: US/09/971,980
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/237,885
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020164349A1e1

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RESULT 9
US-10-437-963-192001
; Sequence 192001, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbaszuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid M
; TITLE OF INVENTION: Plants and Uses Th
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,9
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 192001
; LENGTH: 949
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT45
US-10-437-963-192001

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Query Match      10.7%; Score 114; DB 16; Length 949;
Best Local Similarity 25.7%; Pred. No. 0.8;
Matches 47; Conservative 23; Mismatches 87; Indels 26; Gaps 6;

QY 4 QPSDVSSECDREGRLQPAERPPQLRPGAPTSLSQTEPQCNPEGNHGEGDSCPHGSPQGP 63
DB 205 QPMQYHQSVTQANRQPGVAPRQMNRP-APQOQAPSGNTAPN-----SVTSFKSPQGP 258
QY 64 LAPP-----SPGFATRSPLFIEMRSSLSRSSSGYFSFDTDRSPAPMSCDK--STQTP 117
DB 259 SAVQFCRCNQMGHYARQCP-----QNPITNSCHANGSTARTPTFAAAQSRPSTQAS 310
QY 118 SPPCAFNHYLSAMASMRQAEADMRPEIWIQAELRRIGDEFNAYYARRVFLNNYQAEED 177
DB 311 GGGSRASHNFGGRVNHVHQAETAQAPDVVMGARVFSKIDLRSGYHQLKI-----RSED 364

QY 178 HPR 180
DB 365 IPK 367

RESULT 10
US-10-437-963-196665
; Sequence 196665, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 196665
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(410)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_92495C.1.pap
US-10-437-963-196665

Query Match      10.5%; Score 111.5; DB 16; Length 410;
Best Local Similarity 28.5%; Pred. No. 0.5;
Matches 49; Conservative 10; Mismatches 50; Indels 63; Gaps 9;

QY 17 RQLQPAER-PPQLRPGAPTSLSQTEPQCNPEGNHGEG-----DSCPHGSPQGP----- 64
DB 142 RQSGPARRGPPAHROQAPTRRSRSPSPHP-THPPRGAPCSFGEDSCTWPSCTPLPRHQ 200
QY 65 -----APPASGPFATRSPLFIEMRSS-----PXLHLVLTSPAKKPTNPSPRISPTSPR 255
DB 201 RRRHGCAPAPSAATAASPAAETP-----PXLHLVLTSPAKKPTNPSPRISPTSPR 255
QY 88 LLRSRSSGYFSFDTDRSPAPMSCDKSTQTPSPCAFNHYLSAMASMRQAE 139
DB 256 PLHSSTPG-----AADSPAPAS--RSPSPSPLEALPSRLT--VSIPTAP 299

RESULT 11
US-10-332-065-2
; Sequence 2, Application US/10332065
; Publication No. US20040018504A1
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; GENERAL INFORMATION:
; APPLICANT: BJORN, Sara Petersen et al.
; TITLE OF INVENTION: A METHOD FOR EXTRACTING QUANTITATIVE
; TITLE OF INVENTION: INFORMATION RELATING TO INTERACTIONS BETWEEN CELLULAR
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 3759-0129P
; CURRENT APPLICATION NUMBER: US/10/332,065
; CURRENT FILING DATE: 2003-04-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 886
; TYPE: PRT
; ORGANISM: Aequoria victoria and Homo sapiens
US-10-332-065-2

Query Match      10.5%; Score 111.5; DB 15; Length 886;
Best Local Similarity 27.5%; Pred. No. 1.2;
Matches 47; Conservative 18; Mismatches 67; Indels 39; Gaps 7;

QY 6 SDVSSECDREGRLQPAERPPQL-----RPGAPTSLSQTEPQ-----GNPEGNHG----- 50
DB 49 SDSAERAERERQPHRPIERADAMDTSDRPLGLTRTMSWPSSPHGTGTGSGGAGGSSRRF 108
QY 51 EGDSCPHGSP-OGPLAPPASPGPPATRSPLFIEMRSSLSRSSSGYFSFDTDRSPAPMS 109
DB 109 EAENGFTSPGSRPLDSQASPG-LVLHGAATSQRRSFLYRSDSY-----DMSPKTMS 162
QY 110 CDKSTQTPSPPCQAFNHYLSAMASMRQAEADMRPEIWIQAELRRIGDEFN 160
DB 163 RN-----SSVTSEAHAEADLIVTPFAQVLASLRVRSNFS 196

RESULT 12
US-10-408-765A-261
; Sequence 261, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boia D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261
; LENGTH: 886
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-261

Query Match      10.5%; Score 111.5; DB 16; Length 886;
Best Local Similarity 27.5%; Pred. No. 1.2;
Matches 47; Conservative 18; Mismatches 67; Indels 39; Gaps 7;

QY 6 SDVSSECDREGRLQPAERPPQL-----RPGAPTSLSQTEPQ-----GNPEGNHG----- 50
DB 49 SDSAERAERERQPHRPIERADAMDTSDRPLGLTRTMSWPSSPHGTGTGSGGAGGSSRRF 108
QY 51 EGDSCPHGSP-OGPLAPPASPGPPATRSPLFIEMRSSLSRSSSGYFSFDTDRSPAPMS 109
DB 109 EAENGFTSPGSRPLDSQASPG-LVLHGAATSQRRSFLYRSDSY-----DMSPKTMS 162
QY 110 CDKSTQTPSPPCQAFNHYLSAMASMRQAEADMRPEIWIQAELRRIGDEFN 160
DB 163 RN-----SSVTSEAHAEADLIVTPFAQVLASLRVRSNFS 196
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OM nucleic - nucleic search, using sw model

Run on: November 11, 2005, 19:43:24 ; Search time 166 Seconds
(without alignments)
5874.825 Million cell updates/sec

Title: US-09-508-832-9

Perfect score: 596

Sequence: 1 atggcaagaacacctctctga.....ctggtgtggagaatgcattg 596

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	394.4	66.2	44479	4	US-09-949-016-17176 Sequence 17176, A
2	294	49.3	417	4	US-09-949-016-5434 Sequence 5434, Ap
3	176	29.5	398	4	US-09-621-976-2153 Sequence 2153, Ap
4	113	19.0	477	4	US-09-621-976-2099 Sequence 2099, Ap
5	110	18.5	601	4	US-09-949-016-189929 Sequence 189929, Ap
6	37	6.2	2110	4	US-09-949-016-1105 Sequence 1105, Ap
7	37	6.2	2111	4	US-09-949-016-1173 Sequence 1173, Ap
8	37	6.2	4047	4	US-09-081-385-1173 Sequence 1173, Ap
9	37	6.2	4047	4	US-09-081-385-1173 Sequence 1173, Ap
10	37	6.2	40546	4	US-09-949-016-12847 Sequence 12847, A
11	37	6.2	40546	4	US-09-949-016-12915 Sequence 12915, A
12	36.2	6.1	12787	4	US-09-949-016-16359 Sequence 16359, A
13	36.2	6.1	15141	4	US-09-949-016-14869 Sequence 14869, A
14	36.2	6.1	17740	4	US-09-949-016-13086 Sequence 13086, A
15	36	6.0	7218	1	US-08-232-463-14 Sequence 14, Ap1
16	35.2	5.9	1776	4	US-09-252-991A-10145 Sequence 10145, A
17	35.2	5.9	2097	4	US-09-252-991A-9932 Sequence 9932, Ap
18	35.2	5.9	2163	4	US-09-252-991A-10079 Sequence 10079, A
19	35.2	5.9	146039	4	US-09-949-016-12449 Sequence 12449, A
20	35	5.9	678	4	US-09-902-540-9456 Sequence 9456, Ap
21	35	5.9	15095	4	US-09-902-540-1077 Sequence 1077, Ap
22	34.4	5.8	42610	4	US-09-949-016-13882 Sequence 13882, A
23	33.8	5.7	11002	4	US-09-949-016-17471 Sequence 17471, A
24	33.8	5.7	11002	4	US-09-949-016-17472 Sequence 17472, A
25	33.8	5.7	11002	4	US-09-949-016-17473 Sequence 17473, A
26	33.4	5.6	1167	4	US-09-252-991A-14177 Sequence 14177, A
27	33.2	5.6	3758	4	US-09-799-451-454 Sequence 454, App

c	28	33	5.5	505	4	US-09-621-976-15639	Sequence 15639, A
	29	33	5.5	1464	1	US-08-243-542-5	Sequence 5, Appli
	30	33	5.5	1464	1	US-08-477-407-5	Sequence 5, Appli
	31	33	5.5	1464	1	US-08-484-355-5	Sequence 5, Appli
	32	33	5.5	2913	1	US-08-243-542-7	Sequence 7, Appli
	33	33	5.5	2913	1	US-08-477-407-7	Sequence 7, Appli
	34	33	5.5	2913	1	US-08-484-355-7	Sequence 7, Appli
	35	33	5.5	2923	1	US-08-243-542-6	Sequence 6, Appli
	36	33	5.5	2923	1	US-08-477-407-6	Sequence 6, Appli
	37	33	5.5	2923	1	US-08-484-355-6	Sequence 6, Appli
	38	33	5.5	3167	4	US-09-949-016-3734	Sequence 3734, Ap
	39	33	5.5	3167	4	US-09-949-016-3735	Sequence 3735, Ap
	40	33	5.5	3183	1	US-08-243-542-8	Sequence 8, Appli
	41	33	5.5	3183	1	US-08-477-407-8	Sequence 8, Appli
	42	33	5.5	3183	1	US-08-484-355-8	Sequence 8, Appli
	43	32.8	5.5	31713	4	US-09-949-016-16960	Sequence 16960, A
	44	32.8	5.5	37155	4	US-09-949-016-16945	Sequence 16945, A
c	45	32.6	5.5	1128	4	US-09-252-991A-3879	Sequence 3879, Ap

ALIGNMENTS

RESULT 1
US-09-949-016-17176
; Sequence 17176, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17176
; LENGTH: 44479
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(44479)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17176

Query Match	66.2%	Score	394.4;	DB	4;	Length	44479;
Best Local Similarity	99.7%	Pred. No.	9.1e-120;				
Matches	395;	Conservative	0;	Mismatches	1;	Indels	0;
Gaps	0;						
QY	1	ATGGCAAGCAACCTTCTGATGTAAGTTCTGATGTGACCGGAAGGTAGACAATTGCGAG	60				
Db	2001	ATGGCAAGCAACCTTCTGATGTAAGTTCTGATGTGACCGGAAGGTAGACAATTGCGAG	2060				
QY	61	CCTGGGAGAGGCTCCCGAGCTCAGACTGGGGCCCTTACTCTCCCTACAGACAGAGCCA	120				
Db	2061	CCTGGGAGAGGCTCCCGAGCTCAGACTGGGGCCCTTACTCTCCCTACAGACAGAGCCA	2120				
QY	121	CAAGTATCTCTGAAGCAATCAGGAGTGAAGGGGACAGTCCCGCCAGCCCTTCCCGAGCCCT	180				
Db	2121	CAAGTATCTCTGAAGCAATCAGGAGTGAAGGGGACAGTCCCGCCAGCCCTTCCCGAGCCCT	2180				
QY	181	CAGGCCCGCTGGGCCCGCCAGCTGCCAGCCCTTGCCCTTTTGTCTACAGATCCCGCTTTTC	240				
Db	2181	CAGGCCCGCTGGGCCCGCCAGCTGCCAGCCCTTGCCCTTTTGTCTACAGATCCCGCTTTTC	2240				
QY	241	ATCTTTATGAGAAGATCTCCCTGCTGCTCGATCCTCGAGGGGTATTTCTCTTTTGAC	300				

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Db 2241 ATCTTTATGAGAAGATCTCCCTGCTGCTCATCTCAGTGGGTATTTCTTTTGAC 2300
QY 301 ACAGACAGAGAGCCAGCAGCCCATGAGTTGTGACAAATCAACACAAACCCCAAGTCTCTCT 360
Db 2301 ACAGACAGAGAGCCAGCAGCCCATGAGTTGTGACAAATCAACACAAACCCCAAGTCTCTCT 2360
QY 361 TGCCAGGCTTCAACCACTATCTCAGTGCATGGCT 396
Db 2361 TGCCAGGCTTCAACCACTATCTCAGTGCATGGGT 2396
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RESULT 2

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US-09-949-016-5434
; Sequence 5434, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5434
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5434
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Query Match 49.3%; Score 294; DB 4; Length 417;

Best Local Similarity 100.0%; Pred. No. 1.7e-87; Mismatches 0; Indels 0; Gaps 0; Matches 294; Conservative 0;

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QY 303 AGACAGGAGCCAGCAGCCCATGAGTTGTGACAAATCAACACAAACCCCAAGTCTCTCTTG 362
Db 123 AGACAGGAGCCAGCAGCCCATGAGTTGTGACAAATCAACACAAACCCCAAGTCTCTCTTG 182
QY 363 CCAGGCTTCAACCACTATCTCAGTGCATGGCTTCCATGAGCGAGGCTGAACCTGCAGA 422
Db 183 CCAGGCTTCAACCACTATCTCAGTGCATGGCTTCCATGAGCGAGGCTGAACCTGCAGA 242
QY 423 TATGCGCCAGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 482
Db 243 TATGCGCCAGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 302
QY 483 TTACTATGCAAGAGGATATTTTGAATATTTACCAAGCAGCGGAGACCCACCGAAT 542
Db 303 TTACTATGCAAGAGGATATTTTGAATATTTACCAAGCAGCGGAGACCCACCGAAT 362
QY 543 GGTATCTTACAGCTGTTCAGTTACATTCGCGCTGGTGTGGAGATGCATTG 596
Db 363 GGTATCTTACAGCTGTTCAGTTACATTCGCGCTGGTGTGGAGATGCATTG 416
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RESULT 3

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US-09-621-976-2153
; Sequence 2153, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
```

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 2153

; LENGTH: 398

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 18..239

; NAME/KEY: misc_feature

; LOCATION: 14

; OTHER INFORMATION: n=a, g, c or t

US-09-621-976-2153

Query Match 29.5%; Score 176; DB 4; Length 398;

Best Local Similarity 100.0%; Pred. No. 3.3e-48;

Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGCAAAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAAGGTAGACAAATTGCAG 60
Db 223 ATGGCAAAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAAGGTAGACAAATTGCAG 282
QY 61 CTGCGGAGAGGCGCTCCCGAGCTCAGACCTGGGGGCCCTACCTCCCTACAGACAGAGCCA 120
Db 283 CTGCGGAGAGGCGCTCCCGAGCTCAGACCTGGGGGCCCTACCTCCCTACAGACAGAGCCA 342
QY 121 CAAGGTAATCTGAAGGCAATCACCGAGTGAAGGGGACAGCTGCCCGACGGCAG 176
Db 343 CAAGGTAATCTGAAGGCAATCACCGAGTGAAGGGGACAGCTGCCCGACGGCAG 398
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RESULT 4

```
US-09-621-976-2099
; Sequence 2099, Application US/09621976
; Patent No. 6639063
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; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2

; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 2099

; LENGTH: 477

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 223..372

US-09-621-976-2099

Query Match 19.0%; Score 113; DB 4; Length 477;

Best Local Similarity 99.2%; Pred. No. 3.5e-27;

Matches 124; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 1 ATGGCAAAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAAGGTAGACAA-TTGC 59
Db 223 ATGGCAAAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAAGGTAGACAA-TTGC 282
QY 60 GCCTGCGGAGAGGCGCTCCCGAGCTCAGACCTGGGGGCCCTACTCCCTACAGACAGAGCC 119
Db 283 GCCTGCGGAGAGGCGCTCCCGAGCTCAGACCTGGGGGCCCTACTCCCTACAGACAGAGCC 342
QY 120 ACAAG 124
Db 343 ACAAG 347
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RESULT 5

US-09-949-016-189929
; Sequence 189929, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 189929
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-189929

Query Match 18.5%; Score 110; DB 4; Length 601;
Best Local Similarity 90.6%; Pred. No. 4e-26;
Matches 116; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 394 GCTTCATGAGCAGCTGAACCTCAGATATGCCCCAGAGATATGATGCCCCAAGAG 453
DB 230 GCTTCATGAGCAGCTGAACCTCAGATATGCCCCAGAGATATGATGCCCCAAGAG 289

QY 454 TTGCGCGGTATCGGAGCAGTTTAAACGCTTACTATGAAGGAGGTTTGTGAATAAT 513
DB 290 TTGCGCGGTATCGGAGCAGTTTAAACGCTTACTATGAAGGAGGTTGATGATGTTTCT 349

QY 514 TACCAAGC 521
DB 350 TTACCCGC 357

RESULT 6
US-09-949-016-1105/c
; Sequence 1105, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1105
; LENGTH: 2110
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1105

Query Match 6.2%; Score 37; DB 4; Length 2110;
Best Local Similarity 53.9%; Pred. No. 0.17;
Matches 76; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 64 GCGGAGGCGCTCCCGAGCTGAGACCTGGGGCCCTTACCTCCCTACAGACAGCCACAA 123
DB 715 GCGTTGAATGTCCACCACTCCACTTGGCAGCAGCTCCGCGACAGCTCAGGGCGG 656

QY 124 GGTAACTCTGAAGCAATCAGGAGTGAAGGGGACAGCTGCCCCCAGCGAGCCCTCAG 183
DB 655 CGTCCACTTGTGCGGGGCTCGGGGTCGCGGGGACAGCTGCGGGCTCGGGCGA 596

QY 184 GCGCGCTGGCCCCACCTGCC 204
DB 595 GCGCGCGCTGGCCCCACATGTC 575

RESULT 7
US-09-949-016-1173/c
; Sequence 1173, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1173
; LENGTH: 2111
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1173

Query Match 6.2%; Score 37; DB 4; Length 2111;
Best Local Similarity 53.9%; Pred. No. 0.17;
Matches 76; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 64 GCGGAGGCGCTCCCGAGCTGAGACCTGGGGCCCTTACCTCCCTACAGACAGCCACAA 123
DB 715 GCGTTGAATGTCCACCACTCCACTTGGCAGCAGCTCCGCGACAGCTCAGGGCGG 656

QY 124 GGTAACTCTGAAGCAATCAGGAGTGAAGGGGACAGCTGCCCCCAGCGAGCCCTCAG 183
DB 655 CGTCCACTTGTGCGGGGCTCGGGGTCGCGGGGACAGCTGCGGGCTCGGGCGA 596

QY 184 GCGCGCTGGCCCCACCTGCC 204
DB 595 GCGCGCGCTGGCCCCACATGTC 575

RESULT 8
US-09-081-385-1/c
; Sequence 1, Application US/09081385
; Patent No. 6593456
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, T.
; APPLICANT: Granger, G.A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
; TITLE OF INVENTION: of Use Thereof
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

QY 124 GGTAACTCTGAAGCAATCAGGAGTGAAGGGGACAGCTGCCCCCAGCGAGCCCTCAG 183
DB 655 CGTCCACTTGTGCGGGGCTCGGGGTCGCGGGGACAGCTGCGGGCTCGGGCGA 596

QY 184 GCGCGCTGGCCCCACCTGCC 204
DB 595 GCGCGCGCTGGCCCCACATGTC 575

RESULT 7
US-09-949-016-1173/c
; Sequence 1173, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1173
; LENGTH: 2111
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1173

Query Match 6.2%; Score 37; DB 4; Length 2111;
Best Local Similarity 53.9%; Pred. No. 0.17;
Matches 76; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 64 GCGGAGGCGCTCCCGAGCTGAGACCTGGGGCCCTTACCTCCCTACAGACAGCCACAA 123
DB 715 GCGTTGAATGTCCACCACTCCACTTGGCAGCAGCTCCGCGACAGCTCAGGGCGG 656

QY 124 GGTAACTCTGAAGCAATCAGGAGTGAAGGGGACAGCTGCCCCCAGCGAGCCCTCAG 183
DB 655 CGTCCACTTGTGCGGGGCTCGGGGTCGCGGGGACAGCTGCGGGCTCGGGCGA 596

QY 184 GCGCGCTGGCCCCACCTGCC 204
DB 595 GCGCGCGCTGGCCCCACATGTC 575

RESULT 8
US-09-081-385-1/c
; Sequence 1, Application US/09081385
; Patent No. 6593456
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, T.
; APPLICANT: Granger, G.A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
; TITLE OF INVENTION: of Use Thereof
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

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, OPERATING SYSTEM: Windows
, SOFTWARE: FastSeq for Windows Version 2.0b
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/09/081.385
, FILING DATE:
, CLASSIFICATION:
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: 08/964,747
, FILING DATE: 05-NOV-1997
, APPLICATION NUMBER: 60/030,761
, FILING DATE: 06-NOV-1996
, ATTORNEY/AGENT INFORMATION:
, NAME: Wu, Frank
, REGISTRATION NUMBER: 41,386
, REFERENCE/DOCKET NUMBER: 22000-20577.21
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 650-813-5600
, TELEFAX: 650-494-0792
, TELEX: 706141
, INFORMATION FOR SEQ ID NO: 1:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 4047 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: double
, TOPOLOGY: linear
, MOLECULE TYPE: Genomic DNA
, US-09-081-385-1

Query Match 6.2%; Score 37; DB 4;
Best Local Similarity 52.2%; Pred. No. 0.25;
Matches 82; Conservative 0; Mismatches

Qy 65 CGGAGAGGCCTCCCGAGCTCAGACCTGGGGCCCCCTA
Db 203 CGAGGCGCGCCCCGCGCGGCCCCACGCGCGGCCCCAT
Qy 125 GTAATCCTGAAGGCAATCACGGAGGCTGAAGGGGACAC
Db 143 GAGCTGGCGGCCCCCGAGCTGGAGAGCGCGGCCCGCA
Qy 185 GCCCGCTGGGCCCGCCAGCTGCCAGCCCTGGCCCTTTTGG
Db 83 CCACTCTGGCCCCCGAGCCCCCGCTGTGTCCGAGTGT

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RESULT 9
US-09-081-385-147
Sequence 147, Application US/09081385
Patent No. 6591456
GENERAL INFORMATION:
APPLICANT: Gatanaga, T.
APPLICANT: Granger, G.A.
TITLE OF INVENTION: Factors Altering Tumor Necrosis
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
TITLE OF INVENTION: of Use Thereof
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/081,385
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 08/964,747
; FILING DATE: 05-NOV-1997
; APPLICATION NUMBER: 60/030,761
; FILING DATE: 06-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wu, Frank
; REGISTRATION NUMBER: 41,386
; REFERENCE/DOCKET NUMBER: 22000-20577.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 147:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4047 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 378...1799
; OTHER INFORMATION:
;
; US-09-081-385-147

Query Match          6.2%; Score 37; DB 4; Length 4047;
Best Local Similarity 52.2%; Pred. No. 0.25; Indels 0; Gaps 0;
Matches 82; Conservative 0; Mismatches 75;

QY      65  CGGAGAGGGCTCCCCAGCTCAGAGCTGGGGGCCCTACTCTCCTACAGACAGAGCCACCAAG 124
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      3845 CGAGGCGCGCCCGCGGGCCCAACGCGGGGCCCATCGGAGGCCAGGACTGCCTCCG 3904
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      125  GTAATCTCTGAAGGCAATCACGGAGGTTGAAGGGGACAGCTGCCCCACCGGACGCCCTCAGG 184
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      3905 GAGCTGGCGGCCCGCCAGCCTGGAGGACCGGCCCGCCAGACGCCCTCCAGCCCTCCCCAGC 3964
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      185  GCCCGCTGGCCCCCACCCTGCGAGCCCTCGGCCCTTTTGC 221
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      3965 CCACTCTGGCGCCGCGAGCCCCCGCCCTGTCGAGTGC 4001
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 10
US-09-949-016-12847/c
; Sequence 12847, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12847
; LENGTH: 40546
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12847

Query Match      6.2%; Score 37; DB 4; Length 40546;
Best Local Similarity 53.9%; Pred No. 0.93;
Matches 76; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

64 GCGGAGAGGCGCTCCCCAGCTCAGACCTGGGGGCCCTACCTCCCTACAGACAGCCACAA 123

```

Db 17974 GCGTTGAATGTCACCAAGCTCCACCTTGGCAGCCAGCGTCCGCGACAGCCCTCAGGCGCG 17915
Qy 124 GGTAACTCTGAAGCAATCAGGAGTGAAGGGGACAGTCCCGCCAGCGAGCCCTCAG 183
Db 17914 GGTCACTTGTGCGGGGCTGCGCGTGGCGGGGACAGTCCCGGCTCGGGCGA 17855
Qy 184 GCGCGGCTGGCCCCACCTGCC 204
Db 17854 GCGCGCGGTGCCACATGTC 17834

RESULT 11
US-09-949-016-12915/c
; Sequence 12915, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12915
; LENGTH: 40546
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12915

Query Match 6.2%; Score 37; DB 4; Length 40546;
Best Local Similarity 53.9%; Pred. No. 0.93;
Matches 76; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
Qy 64 GCGGAGAGGCTCCCGACGCTGAGCTGGGGCCCTACTCTCCTACACAGAGCCACAA 123
Db 17974 GCGTTGAATGTCACCAAGCTCCACCTTGGCAGCCAGCGTCCGCGACAGCCCTCAGGCGCG 17915
Qy 124 GGTAACTCTGAAGCAATCAGGAGTGAAGGGGACAGTCCCGCCAGCGAGCCCTCAG 183
Db 17914 GGTCACTTGTGCGGGGCTGCGCGTGGCGGGGACAGTCCCGGCTCGGGCGA 17855
Qy 184 GCGCGGCTGGCCCCACCTGCC 204
Db 17854 GCGCGCGGTGCCACATGTC 17834

RESULT 12
US-09-949-016-16359
; Sequence 16359, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16359

; LENGTH: 12787
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16359
Query Match 6.1%; Score 36.2; DB 4; Length 12787;
Best Local Similarity 51.6%; Pred. No. 0.88;
Matches 83; Conservative 0; Mismatches 78; Indels 0; Gaps 0;
Qy 61 CCTGGGAGAGGCTCCCGACGCTCAGACCTGGGGCCCTACTCTCCTACACAGAGCCA 120
Db 9187 CCTCCCAAGCCCTGCTCTGGCCCTCCCTTGTGAGTACTCTCCCAAGCCCGCTGCA 9246
Qy 121 CAAGGTAATCTCTGAAGCAATCAGGAGTGAAGGGGACAGTCCCGCCAGCGAGCCCT 180
Db 9247 TTCCACAGGCCAAAGCCCTAGTGACAGTTCTTAGGGGACAGGACAGCTAGGGGGCCCC 9306
Qy 181 CAGGCGCGCTGGCCCCACCTGCCAGCGCTGGCCCTTTTGC 221
Db 9307 CAGAGGCCACTAGAGAAACCTGCAGGTGCTGCGCCATCTGGC 9347

RESULT 13
US-09-949-016-14869/c
; Sequence 14869, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14869
; LENGTH: 15141
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14869

Query Match 6.1%; Score 36.2; DB 4; Length 15141;
Best Local Similarity 50.9%; Pred. No. 0.97;
Matches 86; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
Qy 217 TTTGCTACAGATCCCGCTTTTTCATCTTTATGAGAGATCCTCCCTGCTGTCGATCC 276
Db 11806 TATGGACCTGGCTGGGTTTTTTTGTGCTTTGCAGCAATCTCTTAATCTTGGATCC 11747
Qy 277 TCCAGTGGGTATTTCTTTTGACACACAGAGAGCCAGCACCACCATGAGTTGTGACAAA 336
Db 11746 TCCAGAGGGAAGGTCTTCTGGCTTGGCCCTAGGGGACAGAGATGCTGATGTAATA 11687
Qy 337 TCACACAAACCCCAAGTCCTCTTGGCAGGCCCTTCAACCACTATCTCA 385
Db 11686 TCACATGGCTACCATGTACAGAGGACACCACTCCATGAGGGTCTCA 11638

RESULT 14
US-09-949-016-13086/c
; Sequence 13086, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307

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; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13086
; LENGTH: 17740
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13086

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```

Query Match          6.1%; Score 36.2; DB 4; Length 17740;
Best Local Similarity 50.9%; Pred. No. 1.1;
Matches 86; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 217 TTGCTACCATCCCGCTTTCATCTTTATGAGAATCTCTCCCTGCTGTCGATCC 276
Db 12004 TATGCACCTGGCTGGCGGTTTTTTTGTGCTTGCAGCAATCTCTTAATCTGGGATCC 11945

QY 277 TCCAGTGGGTATTTCTCTTTTACACAGACAGAGAGCCACCATGAGTTGTGACAAA 336
Db 11944 TCCACAGGAGAGGTCTTCTGGCTTGGCCCTAGGGGCGAAGATGCTGATGTGAATAA 11885

QY 337 TCACACAAACCCCAAGTCTCTCTTGCAGGCTTCAACCACTATCTCA 385
Db 11884 TCACCATGGCTACCATGTACAGAGACACCACTCCAAATGAGGGTCTCA 11836

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RESULT 15
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)863-4109
; INFORMATION FOR SEQ ID NO: 14:

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14

Query Match          6.0%; Score 36; DB 1; Length 7218;
Best Local Similarity 3.8%; Pred. No. 0.74;
Matches 9; Conservative 138; Mismatches 93; Indels 0; Gaps 0;

QY 162 CTGCCCCACGCGCAGCCCTCAGGGCCGCTGCCCCACCTGCAGCCCTGGCCCTTTTGC 221
Db 1212 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1271

QY 222 TACCAGATCCCGCTTTTCATCTTTATGAGAAGATCCTCCTGCTGCTCGATCCTCAG 281
Db 1272 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1331

QY 282 TGGGTATTTCTCTTTTGACACAGACAGAGAGCCAGCCACCATGAGTTGTGACAAATCAAC 341
Db 1332 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1391

QY 342 ACAAAACCCCAAGTCTCTCTTGCAGGCTTCAACCACTATCTCAGTCAATGGCTTCCAT 401
Db 1392 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1451

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Search completed: November 12, 2005, 05:00:03
Job time : 176 secs

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OM nucleic - nucleic search, using sw model

Run on: November 12, 2005, 03:53:03 ; Search time 738 Seconds
(without alignments)
6678.607 Million cell updates/sec

Title: US-09-508-832-9

Perfect score: 596

Sequence: 1 atggcaagcaacctctga.....ctgggtggagaatgattg 596

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA:**

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US05_PUBCOMB.seq.*
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19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
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21: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
27: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
28: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	314	52.7	536	10	US-09-918-995-31159
2	292.4	49.1	826	20	US-10-755-889-15
3	276	46.3	442	24	US-10-450-763-1154
4	237	39.8	403	10	US-09-918-995-36495
5	110	18.5	455	14	US-10-027-632-75254

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6 110 18.5 455 14 US-10-027-632-313542 Sequence 313542, A
7 110 18.5 455 18 US-10-027-632-75254 Sequence 75254, A
8 110 18.5 455 18 US-10-027-632-313542 Sequence 313542, A
9 105.2 17.7 199 15 US-10-092-750-72 Sequence 72, Appl
10 98.8 16.6 105 15 US-10-092-750-153 Sequence 153, Appl
11 60 10.1 60 10 US-09-908-975-13260 Sequence 13260, A
12 41.4 6.9 653 15 US-10-184-644-402 Sequence 402, Appl
13 41.4 6.9 653 15 US-10-184-644-402 Sequence 402, Appl
14 41 6.9 65 10 US-09-908-975-2414 Sequence 2414, Appl
15 38.6 6.5 55001 18 US-10-160-497-4 Sequence 4, Appli
16 38.6 6.5 55001 18 US-10-348-750-4 Sequence 4, Appli
17 38.6 6.5 55001 22 US-10-991-147-4 Sequence 4, Appli
18 38.4 6.4 1978 19 US-10-425-114-3109 Sequence 3109, Appl
19 38.4 6.4 2233 21 US-10-425-115-182927 Sequence 182927, A
20 37 6.2 410 9 US-09-960-352-11496 Sequence 11496, A
21 37 6.2 615 17 US-10-029-386-24080 Sequence 24080, A
22 37 6.2 2107 9 US-09-981-353-49 Sequence 49, Appl
23 37 6.2 2110 18 US-10-172-118-1846 Sequence 1846, Appl
24 37 6.2 2110 19 US-10-342-887-1846 Sequence 1846, Appl
25 37 6.2 2110 20 US-10-717-597-35 Sequence 35, Appl
26 37 6.2 2110 23 US-10-727-100-382 Sequence 382, Appl
27 37 6.2 4047 9 US-09-752-639-1 Sequence 1, Appli
28 37 6.2 4047 9 US-09-752-639-147 Sequence 147, Appl
29 37 6.2 4047 9 US-09-984-138-1 Sequence 1, Appli
30 37 6.2 4047 9 US-09-984-138-147 Sequence 147, Appl
31 37 6.2 4047 22 US-10-967-092-1 Sequence 1, Appli
32 37 6.2 4047 22 US-10-967-092-147 Sequence 147, Appl
33 37 6.2 4047 26 US-11-011-500-1 Sequence 1, Appli
34 37 6.2 4047 26 US-11-011-500-147 Sequence 147, Appl
35 37 6.2 4047 26 US-11-012-047-1 Sequence 1, Appli
36 37 6.2 4047 26 US-11-012-047-147 Sequence 147, Appl
37 36.8 6.2 480 9 US-09-864-761-1601 Sequence 1601, Appl
38 36.8 6.2 680 20 US-10-437-963-18984 Sequence 18984, A
39 36.6 6.1 65 10 US-09-908-975-28707 Sequence 28707, A
40 36.4 6.1 563 13 US-09-925-065A-810499 Sequence 810499, A
41 36.4 6.1 1318 14 US-10-027-632-84180 Sequence 84180, A
42 36.4 6.1 1318 18 US-10-027-632-84180 Sequence 84180, A
43 36 6.0 5487 16 US-10-156-761-2499 Sequence 2499, Appl
44 36 6.0 9025608 16 US-10-156-761-1 Sequence 1, Appli
45 35.8 6.0 569 9 US-09-864-761-9341 Sequence 9341, Appl
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ALIGNMENTS

```
RESULT 1
US-09-918-995-31159
; Sequence 31159, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31159
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(536)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31159
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Query Match 52.7%; Score 314; DB 10; Length 536;
Best Local Similarity 100.0%; Pred. No. 6e-98; Indels 0;
Matches 314; Conservative 0; Mismatches 0; Gaps 0;

QY 1 ATGGCAAGACCTTCTGATGTAAGTTCTGAGTGTGACCGAGAGGTAGACAATTGCAG 60
Db 223 ATGGCAAGACCTTCTGATGTAAGTTCTGAGTGTGACCGAGAGGTAGACAATTGCAG 282
QY 61 CTGCGGAGAGGCTCCCGAGCTCAGACCTGGGGCCCTTACCTCCCTACAGACAGAGCCA 120
Db 293 CTGCGGAGAGGCTCCCGAGCTCAGACCTGGGGCCCTTACCTCCCTACAGACAGAGCCA 342
QY 121 CAAGTAATCTGAAGGCAATCA CGAGGTGAAGGGGACAGCTGCCCCCAGCGCCTT 180
Db 343 CAAGTAATCTGAAGGCAATCA CGAGGTGAAGGGGACAGCTGCCCCCAGCGCCTT 402
QY 181 CAGGCGCGCTGGCCCACTCCAGCCTGCGCCCTTTGCTACAGATCCCGCTTTTC 240
Db 403 CAGGCGCGCTGGCCCACTCCAGCCTGCGCCCTTTGCTACAGATCCCGCTTTTC 462
QY 241 ATCTTTATGAGAAGATCTCCCTGCTGCTCGATCTCCAGTGGGTATTTCTTTTGAC 300
Db 463 ATCTTTATGAGAAGATCTCCCTGCTGCTCGATCTCCAGTGGGTATTTCTTTTGAC 522
QY 301 ACAGACAGAGGCC 314
Db 523 ACAGACAGAGGCC 536

RESULT 2
US-10-755-889-15
; Sequence 15, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; FILE REFERENCE: D0284 NP
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 826
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-755-889-15

Query Match 49.1%; Score 292.4; DB 20; Length 826;
Best Local Similarity 99.7%; Pred. No. 2.4e-90;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 303 AGACAGAGCCAGCACCACCTGAGTTGTGACAAATCAACACAAACCCCAAGTCTCTTTG 362
Db 123 AGACAGAGCCAGCACCACCTGAGTTGTGACAAATCAACACAAACCCCAAGTCTCTTTG 182
QY 363 CAGGCTTCAACCACTATCTCAGTGCATATGGCTTCCATGAGGAGGCTGAACCTGCAGA 422
Db 183 CAGGCTTCAACCACTATCTCAGTGCATATGGCTTCCATGAGGAGGCTGAACCTGCAGA 242
QY 423 TATGCGCCAGAGATATGATCGCCCAAGAGTTGGCGCTATCGGAGACGAGTTTAAACGC 482
Db 243 TATGCGCCAGAGATATGATCGCCCAAGAGTTGGCGCTATCGGAGACGAGTTTAAACGC 302
QY 483 TTACTATGCAAGAGGGTATTTTGAATAATTACCAAGCAGCGGAGACCAACCCAGAT 542
Db 303 TTACTATGCAAGAGGGTATTTTGAATAATTACCAAGCAGCGGAGACCAACCCAGAT 362
QY 543 GGTATCTTACGACTGTACGTTACATTTCCGCTGGTGTGGAGATGATGATG 596
Db 363 GGTATCTTACGACTGTACGTTACATTTCCGCTGGTGTGGAGATGATGATG 416

RESULT 3
US-10-450-763-1154
; Sequence 1154, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CI33/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 1154
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (167)-(442)
; OTHER INFORMATION: 100% homologous to Homo sapiens BimEL, accession number
; OTHER INFORMATION: AF032457, Smith-Waterman Score=497.
US-10-450-763-1154

Query Match 46.3%; Score 276; DB 24; Length 442;
Best Local Similarity 100.0%; Pred. No. 9e-85;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAGAGGTAGACAATTGCAG 60
Db 167 ATGGCAAGCAACCTTCTGATGTAAGTTCTGAGTGTGACCGAGAGGTAGACAATTGCAG 226
QY 61 CTGCGGAGAGGCTCCCGAGCTCAGACCTGGGGCCCTTACCTCCCTACAGACAGAGCCA 120
Db 227 CTGCGGAGAGGCTCCCGAGCTCAGACCTGGGGCCCTTACCTCCCTACAGACAGAGCCA 286
QY 121 CAAGTAATCTGAAAGCAATCACCGAGGTGAAGGGGACAGCTGCCCCCAGCGCCTT 180
Db 287 CAAGTAATCTGAAAGCAATCACCGAGGTGAAGGGGACAGCTGCCCCCAGCGCCTT 346
QY 181 CAGGCGCGCTGGCCCACTCCAGCCTGCGCCCTTTTGTACAGATCCCGCTTTTC 240
Db 347 CAGGCGCGCTGGCCCACTCCAGCCTGCGCCCTTTTGTACAGATCCCGCTTTTC 406
QY 241 ATCTTTATGAGAGATCTCCCTGCTGCTCGATCC 276
Db 407 ATCTTTATGAGAGATCTCCCTGCTGCTCGATCC 442

RESULT 4
US-09-918-995-36495
; Sequence 36495, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36495
; LENGTH: 403
; TYPE: DNA

US-09-918-995-36495

		Query Match		39.8%; Score 237; DB 10; Length 403;	
		Best Local Similarity		100.0%; Pred. No. 3.1e-71;	
Matches	237; Conservative	0; Mismatches	0; Indels	0; Gaps	0;

QY	1	ATGGCAAGCAACCTTCTGATCTAAGTTGTGAGTGTCGCCGAGAGGTAGACAATTGCAG	60
DB	167	ATGGCAAAAGCAACTTCTCATTAAGTTCTGAGTGTCGCCGAGAGGTAGACAATTGCAG	226
QY	61	CCTCGCAGAGGAGCCCTCCCAGAGTCCAGACCTGGGGCCCCCTACCCTCCCTACACAGAGCCA	120
DB	227	CCTCGCAGAGGAGCCCTCCCAGAGTCCAGACCTGGGGCCCCCTACCCTCCCTACACAGAGCCA	286
QY	121	CAAGGTAATCTGAAGGCAATCACGGAGGTGAAGGGGACAGTGGCCCCCAGCGAGCCCT	180
DB	287	CAAGGTAATCTGAAGGCAATCACGGAGGTGAAGGGGACAGTGGCCCCCAGCGAGCCCT	346
QY	181	CAGGGCCCGCTGGSCCCCACTGCAGCCCTGGCCCTTTTTGTCTACAGATCCCCGCTT	237
DB	347	CAGGGCCCGCTGGSCCCCACTGCAGCCCTGGCCCTTTTTGTCTACAGATCCCCGCTT	403

RESULT 5

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US-10-027-632-75254      ; Sequence 75254, Application US/10027632
                           ; Publication No. US20020198371A1
                           ; GENERAL INFORMATION:
                           ; APPLICANT: Wang, David G.
                           ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
                           ; FILE REFERENCE: 108827.129
                           ; CURRENT APPLICATION NUMBER: US/10/027,632
                           ; PRIOR FILING DATE: 2002-04-30
                           ; PRIOR APPLICATION NUMBER: US 60/218,006
                           ; PRIOR FILING DATE: 2000-07-12
                           ; PRIOR APPLICATION NUMBER: US 60/198,676
                           ; PRIOR FILING DATE: 2000-02-24
                           ; PRIOR APPLICATION NUMBER: US 60/167,363
                           ; PRIOR FILING DATE: 1999-11-23
                           ; PRIOR APPLICATION NUMBER: US 60/156,358
                           ; PRIOR FILING DATE: 1999-09-28
                           ; PRIOR APPLICATION NUMBER: US 60/146,002
                           ; PRIOR FILING DATE: 1999-08-09
                           ; NUMBER OF SEQ ID NOS: 325720
                           ; SOFTWARE: FastSeq for Windows Version 4.0
                           ; SEQ ID NO 313542
                           ; LENGTH: 455
                           ; TYPE: DNA
                           ; ORGANISM: Human
US-10-027-632-313542
    
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		Query Match		18.5%; Score 110; DB 14; Length 455;	
		Best Local Similarity		90.6%; Pred. No. 4.6e-27;	
Matches	116; Conservative	1; Mismatches	11; Indels	0; Gaps	0;

QY	394	GCTTCCATGAGGCGAGCTGAACCTGCAGATATGCGCCAGAGATATGGATGCCCAAGAG	453
DB	79	GCTTCCATGAGGCGAGCTGAACCTGCAGATATGCGCCAGAGATATGGATGCCCAAGAG	138
QY	454	TTCGGCGGTATCGGAGACGAGTTTAAACGCTTACTATGCAAGGAGGTATTTTGAATAAT	513
DB	139	TTCGGCGGTATCGGAGACGAGTTTAAACGCTTACTATGCAAGGAGGTATTTTGAATAAT	198
QY	514	TACCAAAGC 521	
DB	199	TTACCCGC 206	

RESULT 7

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US-10-027-632-75254      ; Sequence 75254, Application US/10027632
                           ; Publication No. US20030204075A9
                           ; GENERAL INFORMATION:
                           ; APPLICANT: Wang, David G.
                           ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
                           ; FILE REFERENCE: 108827.129
                           ; CURRENT APPLICATION NUMBER: US/10/027,632
                           ; PRIOR FILING DATE: 2002-04-30
                           ; PRIOR APPLICATION NUMBER: US 60/218,006
                           ; PRIOR FILING DATE: 2000-07-12
                           ; PRIOR APPLICATION NUMBER: US 60/198,676
                           ; PRIOR FILING DATE: 2000-04-20
                           ; PRIOR APPLICATION NUMBER: US 60/193,483
                           ; PRIOR FILING DATE: 2000-03-29
                           ; PRIOR APPLICATION NUMBER: US 60/185,218
                           ; PRIOR FILING DATE: 2000-02-24
                           ; PRIOR APPLICATION NUMBER: US 60/167,363
                           ; PRIOR FILING DATE: 1999-11-23
                           ; PRIOR APPLICATION NUMBER: US 60/156,358
                           ; PRIOR FILING DATE: 1999-09-28
                           ; PRIOR APPLICATION NUMBER: US 60/146,002
                           ; PRIOR FILING DATE: 1999-08-09
                           ; NUMBER OF SEQ ID NOS: 325720
                           ; SOFTWARE: FastSeq for Windows Version 4.0
                           ; SEQ ID NO 75254
                           ; LENGTH: 455
                           ; TYPE: DNA
                           ; ORGANISM: Human
US-10-027-632-75254
    
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		Query Match		18.5%; Score 110; DB 14; Length 455;	
		Best Local Similarity		90.6%; Pred. No. 4.6e-27;	
Matches	116; Conservative	1; Mismatches	11; Indels	0; Gaps	0;

QY	394	GCTTCCATGAGGCGAGCTGAACCTGCAGATATGCGCCAGAGATATGGATGCCCAAGAG	453
DB	79	GCTTCCATGAGGCGAGCTGAACCTGCAGATATGCGCCAGAGATATGGATGCCCAAGAG	138
QY	454	TTCGGCGGTATCGGAGACGAGTTTAAACGCTTACTATGCAAGGAGGTATTTTGAATAAT	513
DB	139	TTCGGCGGTATCGGAGACGAGTTTAAACGCTTACTATGCAAGGAGGTATTTTGAATAAT	198
QY	514	TACCAAAGC 521	
DB	199	TTACCCGC 206	

; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75254
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-75254

Query Match 18.5%; Score 110; DB 18; Length 455;
Best Local Similarity 90.6%; Pred. No. 4.6e-27;
Matches 116; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
QY 394 GCTTCCATGAGGCGCTGAACCTGCAGATATGCGCCCAAGATATGGATCGCCCAAGAG 453
Db 79 GCTTCCATGAGGCGCTGAACCTGCAGATATGCGCCCAAGATATGGATCGCCCAAGAG 138
QY 454 TTGCGCGTATCGGAGACGAGTTTAAACGCTTACTATGCAAGGAGGTTATTTTGAATAAT 513
Db 139 TTGCGCGTATCGGAGACGAGTTTAAACGCTTACTATGCAAGGAGGTTATTTTCT 198
QY 514 TACCAAGC 521
Db 199 TTACCCGC 206

RESULT 8
US-10-027-632-313542
; Sequence 313542, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313542
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-313542

Query Match 18.5%; Score 110; DB 18; Length 455;
Best Local Similarity 90.6%; Pred. No. 4.6e-27;
Matches 116; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
QY 394 GCTTCCATGAGGCGCTGAACCTGCAGATATGCGCCCAAGATATGGATCGCCCAAGAG 453
Db 79 GCTTCCATGAGGCGCTGAACCTGCAGATATGCGCCCAAGATATGGATCGCCCAAGAG 138
QY 454 TTGCGCGTATCGGAGACGAGTTTAAACGCTTACTATGCAAGGAGGTTATTTTGAATAAT 513
Db 139 TTGCGCGTATCGGAGACGAGTTTAAACGCTTACTATGCAAGGAGGTTATTTTCT 198

QY 514 TACCAAGC 521
Db 199 TTACCCGC 206
RESULT 9
US-10-092-750-72
; Sequence 72, Application US/10092750
; Publication No. US20030032157A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, Philip W.
; APPLICANT: Alpin, Julia
; APPLICANT: Wright, Martin C.
; TITLE OF INVENTION: Polypeptides Interactive with BCL-XL
; FILE REFERENCE: 50036/050002
; CURRENT APPLICATION NUMBER: US/10/092,750
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,526
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 199
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-750-72

Query Match 17.7%; Score 105.2; DB 15; Length 199;
Best Local Similarity 89.7%; Pred. No. 1.5e-25;
Matches 113; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 374 ACCACTATCTCAGTGCATGCTTCCATGAGGAGGCTGAACCTGCAGATATGCGCCCAAG 433
Db 34 ACAATTCCTTACTTCAATGCTTCCATGAGGAGGCTGAACCTGCAGATATGCGCCCAAG 93
QY 434 AGATATGATGCGCCCAAGAGTTGCGCGTATCGGAGACGAGTTTAAACGCTTACTATGCAA 493
Db 94 AGATATGATGCGCCCAAGAGTTGCGCGTATCGGAGACGAGTTTAAACGCTTACTATGCAA 153
QY 494 GAGAGG 499
Db 154 GAGAGG 159

RESULT 10
US-10-092-750-153
; Sequence 153, Application US/10092750
; Publication No. US20030032157A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, Philip W.
; APPLICANT: Alpin, Julia
; APPLICANT: Wright, Martin C.
; TITLE OF INVENTION: Polypeptides Interactive with BCL-XL
; FILE REFERENCE: 50036/050002
; CURRENT APPLICATION NUMBER: US/10/092,750
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,526
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 153
; LENGTH: 105
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-750-153

Query Match 16.6%; Score 98.8; DB 15; Length 105;
Best Local Similarity 98.0%; Pred. No. 1.9e-23;
Matches 100; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 394 GCTTCCATGAGGCGCTGAACCTGCAGATATGCGCCCAAGATATGGATCGCCCAAGAG 453
Db 1 GCTTCCATGAGGCGCTGAACCTGCAGATATGCGCCCAAGATATGGATCGCCCAAGAG 60

Db 430 KRMD.M.TH.THM.A.H.T.TMRRS.TN..M.....CCY.B.A.G.RMYTHYDA.G 371
QY 333 CAATCAACACAAACCCCAAGTCCTCTGCGAGCCCTTCAACCACTATCTCAGTGCAAT 392
Db 370 N.T...H..TMN.SMATR.TCYTB.T.BN.MH...TMNR.NKTHBDYCEM.RHBC.MB 311
QY 393 GCGTTC 398
Db 310 GM.TWS 305

RESULT 14

US-09-908-975-2414
; Sequence 2414, Application US/09908975
; Publication NO. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2414
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-908-975-2414

Query Match 6.9%; Score 41; DB 10; Length 65;
Best Local Similarity 76.9%; Pred. NO. 0.0019;
Matches 50; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 432 ACAGATATCGATCGCCCAAGAGTCGGCGATCGGAGAGGAGTTAAGCTTACTATGC 491
Db 1 ACAGATACCGATCGCACAGAGTCGCGGATCGGAGAGGAGTTCAATGAGACTTACAC 60
QY 492 AAGGA 496
Db 61 GAGGA 65

RESULT 15

US-10-160-497-4/c
; Sequence 4, Application US/10160497
; Publication NO. US20030224513A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Erich Koller
; TITLE OF INVENTION: ANTISENSE MODULATION OF NOTCH1 EXPRESSION
; FILE REFERENCE: RTS-0386
; CURRENT APPLICATION NUMBER: US/10/160,497
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 4
; LENGTH: 55001
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-10-160-497-4

Query Match 6.5%; Score 38.6; DB 18; Length 55001;

Best Local Similarity 51.4%; Pred. NO. 0.25;
Matches 89; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
QY 61 CCTGCGGAGAGGCTCTCCCACTCAGACTGAGCTGGGGCCCTTACTCTCCTTACAGACAGAGCCA 120
Db 12959 CTTCCCCACAGAGCCCCCAGTCTCCCAAGAGCCCCCAGTCTCCCTCCCAAGAGCCCC 12900
QY 121 CAAGGTAATCTGAGGCAATCAGGAGGTGAAGGGGACAGTGCCTCCCAAGAGCCCCCAGGAGCCCT 180
Db 12899 CCCAGTCTCTCCCAACAGAGCCCCCAGTCTCCCTCCCAAGAGCCCCCAGTCTCTCCCA 12840
QY 181 CAGGGCCCGCTGGCCCCCACTGCGAGCCCTGGCCCTTTTGTCTACAGATCCCC 233
Db 12839 CAGAGCCCCCGAGTCTCTCCCAAGAGCCCCCAGTCTCCCTCCCAAGAGCCCCCAGGAGCCCC 12787

Search completed: November 12, 2005, 06:38:21
Job time : 745 secs